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Title:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DEFA5097  LOCUS  DEFINITION  DI-R-C2p-qt-e-07-0-UI.rl  DI-R-C2p Rattus norvegicus cDNA clone  ACCESSION  DEFA5097  VERSION  DEFA5097  VERSION  DEFA5097.1 Gi:l1636204  KEYWORDS  SOURCE  ORGANISH  Rattus norvegicus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  Rattus  Rattus  Reference  AUTHORS  Romalio, M.F., Lennon, G. and Soares, M.B.  Normalization and subtraction: two approaches to facilitate gene  discovery  discovery	RESULT 1	15.8 83.2 464 228 AQ436361 15.8 83.2 481 1 AA036818 15.8 83.2 487 159 N42289 15.8 83.2 494 169 BF743356 15.8 83.2 494 169 BF743356 15.8 83.2 502 229 AQ484899 15.8 83.2 502 229 AQ484899 15.8 83.2 504 105 ALCO9145 15.8 83.2 515 111 AN078344 15.8 83.2 525 235 AQ917005 15.8 83.2 525 235 AQ917005	C 21 15.8 83.2 251 161 BB50/253 BB50/263 B50/263 BB50/263	16.4 86.3 574 104 AIP79827 16.4 86.3 574 104 AIP79827 16.4 86.3 616 247 AZ664475 16.4 86.3 616 247 AZ664475 16.4 86.3 978 173 BG109825 16 84.2 206 17 AIZ03923 16 84.2 348 BAS04455 16 84.2 341 9 AAS77148 15.8 83.2 115 190 W25430 15.8 83.2 132 19 AI36310 15.8 83.2 133 19 AI36310 15.8 83.2 135 163 BE142610 15.8 83.2 136 HE142610 15.8 83.2 137 144 AW366100	Query Query e Match Length DB ID e Match 152 150 BF545097 4 91.6 522 150 BF545097 4 91.6 608 230 ACC540572 7 89.5 367 115 AW29811 7 89.5 936 175 BG297415 8 86.3 356 223 ACC68059
RESULT 2 AQ540572/c LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Similarity 94.7%; Pred. No. 2.1e+02; 8; Conservative 0; Mismatches 1; 1   1   1   1   1   1   1   1   1	NT 19	library is a subtracted library derived from the UI-R-CI library, which is a subtracted library derived from the UI-R-CO library. The UI-R-CO library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8.12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dor track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The	This LLNL Seq   Surce	JOURNAL Genome Res. 6 (9), 791-806 (1996)  MEDLINE 97044477  CONTACT: Soares, MB  Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250  Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)

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JOURNAL
COMMENT
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                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -min
                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                          Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 367)
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FORWARD: AGGAAACAGCTATGACCATBACKWARD: GTTTTCCCAGTCACGACG
                                           PCR PRimers
                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW429811 367 bp mrNA EST 68306 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                 Tel: 402 762 4366
Fax: 402 762 4390
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville,
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Seq primer: T7
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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83 c 93 g 173 t
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/clone="RPCI-11-358E23"
/clone_lib="RPCI-11"
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/db_xref="GDB:7637206"
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Location/Qualifiers
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Plate: LLAM10383 row
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Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG297415.1 GI:13061044
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Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nouse mouse
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              /tissue_type="retina"
/lab_host="Diagnation" | /the host="Diagnation of the light o
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/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:4507022"
/clone_lib="NIH_MGC_94"
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). 3.1e+02;
ches 0;
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from day 11, 13, 15, 20,
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Query Match 89.5%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 3.1 Matches 17; Conservative 0; Mismatches

Score 17; Pred. No.

DB 175; 3.6e+02;

Length

936;

Indels

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                 88888
88888
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|: /SIDS1/gcgdati
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/SIDS1/gcydata/geneseq/geneseqn/NA1991.DAT:*

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/SIDS1/gcgdata/geneseg/genesegn/NA1985.DAT:*
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4 21 AAD00564
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73 19 AAY70310
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AAZ45110
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Streptococcus pyog
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                                                                                                                                                  UGT1*1 gene exon 1
UDP-glucuronosyltr
UGT1A Exon 1 from
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                                                                                                                                      HUG-Br1.
                                                                                                                                  Homo sap
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n secreted	encod	EST DNA43		5	nucleotic			colon car		Human secreted pro		protein	secret	fruit ri	Human secreted pro	Polynucleating se	Ω	Nucleotide sequenc	tide	gene		e :	Gastric cancer	_	ž :	n signal	Human secreted	שלים שחום	5 isoform	Sisoform		5 isoform	LRP5 isoform 1	

## ALIGNMENTS

DR WPI, 19 XX Improvi			PR 16-MAR-1996; PR 01-MAR-1996;	PF 03-MAR-1997;	PD 04-SEP-1997	XX PN W09732042-A2	OS Synthetic. OS Homo sapiens.		XX Uridine		AC AAT79542;	ID AAT795
<pre>WPI, 1997-448702/41. Improving drug trial efficiency comprises identifying participants</pre>	Burchelle B	(UYDU-) UNIV DUNDEE.	1996; 96GB-0005598. 1996; 96GB-0004480.	1997; 97WO-GB00577.	1997.	)42-A2.	ic. piens	Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; billrubin glucuronidation; Crigler-Najjar; type 2; drug metabolism; brug trial efficiency; screening; PCR primer; ss.	Uridine diphosphate glucuronosyltransferase gene: UGT:	-1998 (first entry)	42;	AAT79542 standard; DNA; 21 BP.

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                              New nucleic acid representing polymorphisms in the human uridine diphosphate glucuronosyltransferase gene, used for diagnosis and evaluation of drug metabolism
            Examples; Page 27-29; 63pp; English
                                                                                                                                WPI; 2000-052981/04.
P-PSDB; AAY57093.
                                                                                                                                                                                                                                                                    07-MAY-1998;
                                                                                                                                                                                                                                                                                                       04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                  W09957322-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe; glucuronic acid; Crigler Najjar syndrome; Gilbert syndrome; jaundice; unconjugated hyperbilirubinaemia; drug metabolism; transgenic animal; pharmacogenetic screening; diagnose; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UDP-glucuronosyltransferase 1 (UGT1) exon 1A nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 12; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with Gilbert's syndrome - useful as their altered drug metabolism may hinder result interpretation
                                                                                                                                                                                       Penny L,
                                                                                                                                                                                                                           (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                              11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        basis of them possessing or not possessing GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 BP; 6 A; 6 C; 4 G;
                                                                                                                                                                                       Galvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                  9805-0084807.
                                                                                                                                                                                                                                                                                                       99WO-US09702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 18;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC Nucleotide sequences AAZ45110-Z45118 are exons 1A-1J of the human CC uridine diphosphate-glucuronosyltransferase I (UGT1) gene. The UGTs are a CC family of enzymes that catalyse the glucuronic acid conjugation of a wide CR range of endogenous and exogenous substrates including phenois, actalyse the substrates including phenois. CC result in toxic substances being converted to compounds which are more CR vater soluble and are excreted. The invention relates to and identifies CR UGT1 polymorphisms (AAZ45004-Z45041). The polymorphisms sequences are CR useful as probes for detecting UGT1 locus polymorphisms, indicative of CR altered UGT1 expression or activity. These polymorphisms are associated CR with Crigler-Najjar and Gilbert syndromes (unconjugated thyperbilirubinamia) and drug metabolism. The genotyping of the UGT1 gene is used to predict the rate of metabolism of UGT1 substrates, possible drug-drug interactions and adverse side effects (i.e. to optimize drug consequences, including polymorphisms, can also be used to produce the CR corresponding protein (or its fragments) or to generate transgenic animals or modified cells e.g. for pharmacogenetic screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "UGITA Exon 1 from the UGIT gene locus
          10-JAN-1992;
                                             06-AUG-1992
                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UGTIA; UGTIBP; UGTIC; UGTID; UGTIE; UGTIF; isozyme; bilirubin; UDP-glucuronosyl transferase; CN; ss.
                                                                           W09212987-A
                                                                                                                                                                                                                                                                                                          TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ33024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ33024 standard; DNA; 1167 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 864 BP; 185 A; 236 C; 209 G; 234 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 CCACTGGGATCAACAGTATCT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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            92WO-US00282
                                                                                                                                                                                                                       /"cag" c
/label= UGT1A_Exon_1
181..909
                                                                                                         /note= "representation of 5 kbp of
non-sequenced DNA between the sequences
represented in AAQ33024 and AAQ33025"
                                                                                                                                                                                                                                                                                                                         /note- "representation of 11.7 kbp of non-sequenced DNA between the sequences represented in AAQ33023 and AAQ33024"
                                                                                                                                                                         /*tag= id
/note= dencodes transferase isoform; see
1148...1167
                                                                                                                                                                                                                                                                               /*tag=
166..9
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                               .909
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Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 4
AAQ27369/c
ID AAQ27369;
XX AAQ27369;
XC AAQ27369;
XX 27-JAN-1993 (first
XX B111rubin; UDP-glucu
KW B111rubin; UDP-glucu
KW monoglucuronide; dig
XX Homo saplens.
XX Loca
FH Key Loca
FH Key Loca
FH Key 16...
FT CDS
FT CDS
FT PolyA_signal 2330
FT polyA_signal 2330
FT polyA_signal 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (2) Exon 2, represented in AAQ33025;
(3) Exon 3, represented in AAQ33025;
(4) Exon 4, represented in AAQ33026;
(5) Exon 5, represented in AAQ33027; and
(6) about 69 kb of non-sequenced DNA.
(6) about 69 kb of non-sequenced by
(7) the six different first exons and identical C-termini of 246 amino
(8) acids are encoded by the common exons 2-5. The UGT1 gene locus
(9) encodes a family of UDP-glucuronosyl transferase isozymes, two of
(9) which metabolise bilirubin.
(10) Patients having Crigler-Najjar Syndrome (CN) Type I, have a
mutation present in the second common exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and II
                                                                                                                                                                                                                                                                                                                                         Bilirubin; UDP-glucuronosyltransferase; HUGBr1; HUGBr2; monoglucuronide; diglucuronide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The isolated gene locus, UGT1, has a sequence of about 10000 by which represent (1) Exon 1, comprising 6 transcriptional units (UGT1F, E. D. C. BP and A), represented in AAQ27368 and AAQ33020-24 respectively:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1167 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1F; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Owens IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 CCACTGGGATCAACAGTATCT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1992-284593/34.
DB; AAR30194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 1: llarity 100.0%; Pred. No. 0.19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9108-0639453.
                                                                                                                                                              /*tag- b
/number- 1
                                                                                                                                                                                               /*tag= a
2330,.2335
                                                                                                                                         2338..2343
                                                                                                      'number-
                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 A; 259 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 G; 340 T; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AAD00564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 21
  Bjorck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                    GRAB protein; protein G related alpha2M binding protein; vaccine, alpha2-macroglobulin; group A Streptococcus; GAS; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The cDNAs contain identical 3' ends (1469 bp in length) to each other and to that of the human phenol transferase cDNA, HLUGP1 (Harding et al., Proc. Natl. Aca. Sci. USA 85:8281 (1988)). In contrast, they have unique 5' ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Two human liver bilirubin UDP-glucuronosyltransferase cDNAs have been isolated. They are referred to as HUGBri (AAQ27369) and HUGBr2 (AAQ27370) (Ritter, et al., J. Biol. Chem. 266:1043-1047 (1991)) and upon expression individually in COS-1 cells, encode isoforms that catalyse the formation of the two bilirubin monoglucuronides and
                                                                                                                      02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes strain KTL3 partial GRAB protein encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and II
                                         (ACTI-) ACTINOVA LTD.
                                                                               02-NOV-1998;
                                                                                                                                                              11-MAY-2000.
                                                                                                                                                                                                   WO200026240-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD00564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD00564 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2351 BP; 602 A; 540 C; 556 G; 653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 9A-I; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-284593/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Owens IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                 immune response; Streptococcus pyogenes infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the diglucuronide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ritter JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEPT HEALTH & HUMAN SERVICE.
    Rasmussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                               98GB-0023975
                                                                                                                      99WO-GB03631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9105-0639453
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                                                                                                                                                                                                                                /product= "GRAB protein"
/partial
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
    X
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Pred. No. 0.2
0; Mismatches
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0.21;
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                                                        05-AUG-1997;
05-AUG-1997;
05-AUG-1997;
05-AUG-1997;
                                                                                                                                                                         05-AUG-1997;
05-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                       Secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality, foetal deficiency; blood disorder; cons disorder; immune system disease; autoimmune disease; hepatic disease; renal disease; diabetes; inflammation; allergy; ischemic shock; hizheimer's; cognitive disorder; schizophrenia; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response against group A Streptococcus. Antibodies against GRAB are useful for treating Streptococcus pyogenes infections. The protein is also useful for purifying alpha2M from a sample. The present sequencies a DNA encoding partial GRAB protein from S. pyogenes strain KTL3. The protein has alpha2M binding region and is useful in vaccine
                                                                                                                  05-AUG-1997
                                                                                                                                                          05-AUG-1997
                                                                                                                                                                                                                                  04-AUG-1998;
                                                                                                                                                                                                                                                            18-FEB-1999
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                              prostate disease; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX30352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 504 BP; 188 A; 97 C; 108 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses a new family of proteins termed GRAB (protein G related alpha2M binding protein) from Streptococcus pyogenes which have the ability to bind alpha2-macroglobulin (alpha2M) and show homology to protein G of group G Streptococcus. GRAB protein and peptides derived from it are used in vaccine compositions for generating a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New alpha2M binding protein for generating a protective immune response to group A streptococcus and purifying the binding protein \,\cdot\,
                                                                                                                                                                                                                                                                                       WO9907891-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses a new family of proteins termed GRAB (protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY71046.
                                                                                                                                                                                                     19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 agtgggttcaacagtatct 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 actgggatcaacagtatct 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 65; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
97US-0054809.
97US-0055310.
97US-0055311.
97US-0055312.
97US-0055316.
97US-0055311.
97US-0055970.
                                                                                                              970S-0054806.
970S-0054807.
970S-0054808.
                                                                                                                                                                         970S-0054798
970S-0054803
                                                                                                                                                                                                                               98WO-US16235.
                                                                                                                                                          97US-0054804
                                                                                                                                                                                                   97US-0056732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 697 BP
                                                                                                                                                                        0054803
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89.5%;
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Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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CC polyniclectides which are useful for preventing, treating or ameliorating conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the secreted polypeptides in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each cof the products, based on which tissues they are most highly compressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, cNS disorders, abnormalities and foetal deficiencies, blood disorders, CNS disorders, cdiseases of the immune system, autoimmune diseases, hepatic and renal cdisease, diabetes, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, cardiovascular disorders, prostate diseases, arthritis or malignancies, diseases of testes, lung or thomus, digestive/endocrine disorders, infections and AIDS. The collyward lase are also messel, for identifications and AIDS. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
Sequence 697 BP; 233 A; 121 C; 171 G; 169 T; 3 other;
                                   polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                 The specification describes secreted proteins and their corresponding
                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 247; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis and treatment of pathalogical diseases
                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes encoding secreted polypeptides - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-167452/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brewer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN
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19-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9705-0056365.
9705-0056366.
9705-0056557.
9705-0056370.
9705-0056371.
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970S-0056731
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Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greene JM,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young
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Young PE,
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                                                                                                                                                                                                                                                                                                               or ameliorating
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RESULT
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                                                                                                                                             Bacillus thuringiensis MIS-6 insecticidal toxin 196F3 DNA
                                                                                                                                                                                                                       AAV30310;
                                                      Bacillus thuringiensis strain PS196F3 (NRRL B-21872)
                                                                                         biological control; lepidopteran; coleopteran; ss.
                                                                                                            Insecticide; pesticide; toxin; MIS-6; delta-endotoxin;
                                                                                                                                                                                    28-SEP-1998
                                                                                                                                                                                                                                                        AAV30310 standard; DNA; 1073 BP
                                                                                                                                                                                                                                                                                                                                                 274 cacagggaacaacagtatc 292
                                                                                                                                                                                                                                                                                                                                                                                    2 cactgggatcaacagtatc 20
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                  (first entry)
Location/Qualifiers 2..1072
                                                                                                                                                                                                                                                                                                                                                                                                                                      75.2%;
89.5%;
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Pred. No. 77
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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> В 20;

Length 697;

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07-MAY-1998 W09818932-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC This DNA sequence encodes a novel soluble toxin (see AAW6027) of CB Bacillus thuringlensis (B.t.) strain PS196F3 (NRRL B-21872). This CC toxin belongs to the novel MIS-6 family of B.t. toxins that have coxicity against non-mammalian pests. The novel DNA was obtained DY PCR amplification (see AAW30288-99) of toxal cellular genomic DNA. It can used to produce recombinant hosts (preferably plant CD DNA. It can used to produce recombinant hosts (preferably plant CD DNA. It can used to produce recombinant hosts (preferably plant CD DNA. It can used to produce recombinant hosts (preferably plant CD DNA. It can used to produce recombinant hosts (preferably plant CD DNA. It can used to produce solution, or as a PCR primer or hybridisation probe for use in identifying and characterising CD DNA is a post of the control of the control of toxins (see AAW60218-32) which have activity against CD DNA toxins (see AAW60218-32) which have activity against CD DNA toxins (see AAW60218-32) which have activity against CD DNA toxins (see AAW60218-32) and AAM9973-87), and transformed host CD CO DNA toxins are also useful to their ability to form pores in cell membranes, and can be used to for their ability to form pores in cell membranes, and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                          15-APR-1998,
                                                                                                                                                                               endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis;
                                                                                                                                                                                                                                             LRP5 isoform 2 longest open reading frame (also isoform 4,5,6).
                                                                                                                                                                                                                                                                                        10-FEB-1999
                                                              22-OCT-1998
                                                                                                W09846743-A1
                                                                                                                                Homo sapiens
                                                                                                                                                               hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss
                                                                                                                                                                                                                 LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
                                                                                                                                                                                                                                                                                                                          AAV70397
                                                                                                                                                                                                                                                                                                                                                       AAV70397 standard; cDNA; 4351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1073 BP; 380 A; 201 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis isolates - used for producing pesticidal toxins and nucleotide sequences for control of lepidopterans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 90; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coleopterans
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                                                                                                                                                                                                                                                                                                                                                                                                                                           838 actgggaaaaacagtatct 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                facilitate entry of a second agent into a target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                     (first entry)
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                          98WO-GB01102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.2%;
89.5%;
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Schnepf HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 82
                                                                                                                                                                                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 G;
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schwab G, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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(WELL ) WELLCOME TRUST LTD.

05-JUN-1997;

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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                        LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1716 cactgggaccaacagaatc 1734
                                                          05-JUN-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor related protein, previously designated LRP-3) isoform 2 CDNA. Nucleic acid molecules (NRMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Allheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and
                                                                                                                                      22-OCT-1998
                                                                                                                                                                   W09846743-A1
                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                        LRP5 cDNA longest open reading frame
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                                                                                                                                                                                                                                                                                                                                                                                                    AAV70395 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hey P, K
                                                                                                       15-APR-1998;
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Hey P, Kawaguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents LRP5 (low density lipoprotein (LDL) recentor related protein, previously designated LRP-3) isoform 2 cb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Fig lib; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-594573/50.
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                                                        970S-0048740
970S-0043553
                                                                                                       98WO-GB01102
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                                                                                                                                                                                                                                                                                                                                                                                                    CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerhold D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                    4843 BP
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Pred. No. le+(
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1309 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      732 T; 0 other;
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数の対象のの政策

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В
            Hey P, K
Phillips
                                                                                                                                                                                                                                                                                     endocytosis; insulin dependent diabetes meilitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases, such as glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the longest open reading frame of LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3) CDNA from the present invention. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated LDL-receptor related protein - used to develon treating, e.g. elevated triglyceride levels, diabetes autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                          Homo sapiens
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                                                                       (MERI ) MERCK & CO INC.
(WELL ) WELLCOME TRUST LTD.
                                                                                                                     05-JUN-1997;
15-APR-1997;
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                                                                                                                                                                                                22-OCT-1998.
                                                                                                                                                                                                                             WO9846743-A1.
                                                                                                                                                                                                                                                                                                                               LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
                                                                                                                                                                                                                                                                                                                                                              LRP5 isoform 3 putative open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4843 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug screening.
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nes 17; Conserv
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      CT, Cox RD, Ger
Kawaguchi Y, Me
''e Todd JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CT, Cox RD,
Kawaguchi Y,
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                                                                                                                    97US-0048740
97US-0043553
                                                                                                                                                               98WO-GB01102
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           Y, Gerhold D, Han
Y, Merriman TR,
JA, Twells RCJ;
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89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8;
Pred. No. 1
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                           R, Metzker ML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ق</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       811 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hess JW;
                                             Hess JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to develop products diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa Y;
                           Nakagawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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cc receptor related protein, previously designated LRP-3). The present CC sequence represents the putative open reading frame of LRP5 isoform 3. CC Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining CC if an individual is susceptible to insulin dependent diabetes mellitus CC (IDM). The NAMS or proteins can be used for reducing triglyceride levels CC useful in the treatment of autoimmune diseases such as CC glomerulonephritis, diseases and disorders involving disruption of condections and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, contamination, pathogenic bacterial toxin contamination, contamination, osteoporosis, Alzheimer's disease and cardiovascular disease. Products CC drug screening.
  New isolated LDL-receptor related protein - used to develop for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 12c; 200pp; English.
Sequence 4915 BP; 992 A; 1614 C; 1474 G; 835 T; 0 other;
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Query Match
Best Local Similarity
watches 17; Conserva B 2279 2 cactgggatcaacagtatc cactgggaccaacagaatc Conservative 75.2%; 20 0 Score 15.8; DB Pred. No. 1e+02; Mismatches 19; Indels Length 4915; 0 0;

AAV85549 LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritus; infiammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; s: W09846743-A1. LRP5 isoform 5 cDNA. 10-FEB-1999 AAV85549; AAV85549 standard; cDNA; 5022 Homo sapiens 11 (first entry) ВÞ lipoprotein; ss

22-OCT-1998

05-JUN-1997; 15-APR-1997; 15-APR-1998; 97US-0048740. 97US-0043553. 98WO-GB01102

Phillips MS, (MERI ) MERCK & CO INC. Kawaguchi Cox RD, Todd JA, Gerhold D, Merriman TR, Twells RCJ; Hammond H, He R, Metzker ML, Hess Nakagawa

WPI; 1998-594573/50

New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes,

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RESULT 1
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A CONTRACTOR AND A CONT
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                                                                                                                                                                                                                                                             Caskey CT, Cox RD, G
Hey P, Kawaguchi Y, I
Phillips MS, Todd JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease, Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents the LRP5 isoform 5 cDNA.

Nucleic acid molecules (NAMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride level in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as
                                                                                New isolated LDL-receptor related protein - used to develop products for treating. e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2178 cactgggaccaacagaatc 2196
                      Claim 3; Fig 5a; 200pp; English.
                                                                                                                                                                                                       WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRP5 isoform 1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV70396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV70396 standard; cDNA; 5098 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5022 BP; 1036 A; 1606 C; 1503 G; 877 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glomerulonephritis, diseases and disorders involving disruption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Fig 14; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                        (WELL )
                                                                                                                                                                                                                                                                                                                                                                                                                     (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 cactgggatcaacagtatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention can also be used for detection, diagnosis and \ensuremath{\operatorname{screening}} .
                                                                                                                                                                                                                                                                                                                                                                                        WELLCOME TRUST LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0048740.
97US-0043553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-GB01102
                                                                                                                                                                                                                                                             , Gerhold D, Han
Y, Merriman TR,
JA, Twells RCJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.2%;
89.5%;
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Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                 Hammond K,
                                                                                                                                                                                                                                                                                                 Metzker ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                              Hess JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                    Nekagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5022;
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The present invention describes LRPS (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). The present sequence represents the LrpS isoform 3 cDNA.

Nucleic acid molecules (NAMs) encoding LRPS can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus

Example 1; Fig 12a; 200pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                          Caskey CT, Cox RD, Gerhold D, He Hey P, Kawaguchi Y, Merriman TR, Phillips MS, Todd JA, Twells RCJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contemination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Froducts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3) isoform 1 cDNA. Nucleic acid molecules (NAMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMs or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be
                                                                                                                                  for treating, e.g. elevated trigiyo autoimmune disorders, inflammation
                                                                                                                                    New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                          WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endocytosis; insulin dependent diabetes mellitus; autoimmune disease;
glomerulonephritis; inflammation; viral infection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV86019 standard; cDNA; 5125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypercholesterolemia; Alzheimer's disease; low density lipoprotein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lrp5 isoform 3
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(WELL ) WELLCOME TRUST LTD.
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97US-0043553.
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Pred. No. 16
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                                                                                                                                                                                                                                                                                 Hammond H,
                                                                                                                                                                                                                                                                Metzker ML,
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AAV85550
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 useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving d
                           Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride level in the serum of an individual. Therapies that affect LRP5 may also be
                                                                                                                                                                                                                                                                                                         Caskey CT, Cox RD, G
Hey P, Kawaguchi Y, I
Phillips MS, Todd JA,
                                                                                                                                                                                                New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocytosis; insulin dependent dia glomerulonephritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IDDM). The NAMS or proteins can be used for reducing triglyceride levels in the serum of an individual. Theraples that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of
                                                                                                 receptor related protein, previously designated sequence represents the LRP5 isoform 6 cDNA.
                                                                                                                                                                    Claim 7; Fig 15a; 200pp; English.
                                                                                                                                                                                                                                                                            WPI; 1998-594573/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5125 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and from the present invention can also be used for detection, diagnosis and from the present invention can also be used for detection,
                                                                                                                                   The present invention describes LRP5 (low density lipoprotein (LDL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypercholesterolemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
endocytosis; insulin dependent diabetes mellitus; autoimmune disease;
glomerulonephritis; inflammation; viral infection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRP5 isoform
                                                                                                                                                                                                                                                                                                                                                                             (WELL ) WELLCOME TRUST LTD.
                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0048740.
97US-0043553.
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                                                                                                                                                                                                                                                                                                         , Gerhold D, Ham
Y, Merriman TR,
JA, Twells RCJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                         Hammond H, He
R, Metzker ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898 T;
involving disruption
                                                                                                                                                                                                                                                                                                                                             Hess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                               LRP-3). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection, diagnosis and
                                                                                                                                                                                                                                                                                                                           Nakagawa
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                              be be
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receptor related protein, previously designated LRP-3). The present sequence represents the LRP5 isoform 2 Day Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NAMS or proteins can be used for reducing triglyceride level in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of endovrous and anticommune content of autoint and disorders involving disruption of endovrous and anticommune proteins and the present and the content of anticommune diseases and the present and the p

levels be

The present invention describes LRP5 (low density lipoprotein (LDL)

Claim 8; Fig 11a; 200pp; English.

New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease

WPI; 1998-594573/50

Caskey CT,

Gerhold D,

Hammond H, Metzker

Hess JW;

Nakagawa

Merriman TR, , Twells RCJ;

Kawaguchi Cox RD,

Todd JA,

(MERI ) MERCK & CO INC.

05-JUN-1997; 15-APR-1997;

97US-0048740 97US-0043553 98WO-GB01102

15-APR-1998; 22-OCT-1998 WO9846743-A1 Homo sapiens

endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elavation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products

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RESULT
ANY85551
ID AAV
AC AAV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRP5
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_ba2:*
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	9b.htg9: ** 9b.htg11: ** 9b.htg11: ** 9b.htg11: ** 9b.htg11: ** 9b.htg11: ** 9b.htg12: ** 9b.htg12: ** 9b.htg12: ** 9b.htg13: **	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1 CCACTGGGATCAACAGTATCT 21
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                                                                                                                        Other publication AU 2224197 19970916.
Location/Qualifiers
                                                                                                                                            UNIV DUNDEE (GB)
                                                                                                                                                   DRUG TRIAL ASSAY SYSTEM
Patent: WO 9732042-A 2 04-SEP-1997;
                                                                                                                                                                                                 unidentified
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230541 Avian infec
M94356 Avian infec
M95169 Avian infec
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AL033125 Drosophil
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AL162632 Homo sapi
AL158062 Homo sapi
AL157833 Homo sapi
AL1579977 Human DNA
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AC025598 Homo sapi
AC060771 Homo sapi
AL139354 Homo sapi
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AL425875 clone BAO
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AC054151 Giardia i
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repeat_region
ary57220 292 bp DNA PRI 27-MAR-2001
Homo sapiens bilirubin UDP-glucuronosyltransferase 1 (UGT1) gene, UGT1+1 allele, promoter and partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McKie, K., Addington, T., Nguyen, T.S., Glendenning, M., Kutlar, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 292)
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                                                                                                   h 100.0%; Score 21; DB 89; Length 292; Similarity 100.0%; Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McKie, K., Addington, T., Nguyen, T.S.,
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                                                                                 Conservative
                                                                                                                                                                                                         /protein_id="AAK27223.1"
/db_xref="GI:i3448829"
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a 69 c 95 g 68 t
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/product="bilirubin UDP-glucuronosyltransferase 1"
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/map="2q37"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-"polymorphic region'
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 RESULT 4
AF180372/C
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AF352795/c
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                                                                    439 CCACTGGGATCAACAGTATCT 419
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                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF352795 531 bp DNA PRI 10-APR-2001 Homo sapiens bilirubin UDP-glucronosyltrasferase 1-1 (UGT1A1) gene, UGT1A1*1 allele, partial cds.
AF352795 AF352795.1 GI:13569708
     Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laboratory, M College of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 531)
McKie,K., Kutlar,F., Glendenning,M. and Kutlar,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                            /codon_start=1
/product='bilirubin UDP-glucronosyltrasferase 1-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="repeat polymorphism compared to UGTIA1 sequence presented in GenBank Accession Number AF180372; contains 7 ta repeats frequently detected in patients with high bilirubinemia"
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<1, .>531
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279. .>292
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279, .295
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                                                                                                                                                                                                                                                                                                                                                                                                                              product="bilirubin UDP-glucronosyltrasferase 1-1"
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/chromosome="2"
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                                                                                                                                            100.0%; Score 21; DB 8
100.0%; Pred. No. 0.73;
tive 0; Mismatches
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OCUS AF180372 541 bp

AF180372

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05-OCT-1999

RESULT 5 AF110194/c

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                      ccactgggatcaacagtatct 21
CCACTGGGATCAACAGTATCT 415
                                                                          ch 100.0%; Score 21; DB 89; Similarity 100.0%; Pred, No. 0.73; 21; Conservative 0; Mismatches 0;
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1 (bases 1 to 54)

Kutlar,F., Sromek,E., Leithner,C., Nechtman,J. and Kutlar,A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with sickle cell anemia upphilished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GA 30912, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-1999) Medicine, Hematology/Oncology-Sickle Cell Center, Medical College of Georgia, 15th Street, AC-1000, Augusta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 541)
Kutlar, F., Sromek, E., Leithner, C., Nechtman, J. and Kutlar, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens bilirubin UDP-glucuronosyltransferase 1-1 (UGT1) gene, UGT1*1 allele, partial cds.
AF180372
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                                                                                                                                                                                             123
                                                                                                                                                                                   /translation~"MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
GAIQQLQQRGHEIVVLAPDASLYIRDG"
a 124 c 141 g 153 t
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/protein_id="AAF01205.1"
/db_xref="GI:6010650"
                                                                                                                                                                                                                                                                                                                              /note-"UDP glycosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"Ritter, J.K., 67:3257-3261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="UGT1"
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/db_xref="taxon:9606"
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/tissue_type="whole blood"
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      et al., 1992,
                                                                                                            Length 541;
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Ritter, J.K., Chen, F., Sheen, Y.Y.,
Yeatman, M.T. and Owens, I.S.
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1190)
Ritter, J.K., Crawford, J.M. and Owens, I.S.
Cloning of two human liver bilirubin UDP-glucuronosyltransferase JNAs with expression in COS-1 cells Johnson. 266 (2), 1043-1047 (1991)
                                                                                                                                                                                                                                                                                                                                              bilirubin UDP-glucuronosyltransferase; isozyme. Homo sapiens (tissue library: cosmid) liver DNA Homo sapiens
                                                                                                       91093210
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Human bilirubin UDP-glucuronosyltransferase (UGTIA) gene isozyme
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Direct Submission
Submitted (01-DEC-1998) Center for Cancer Research, MIT,
Submitted Research, MIT,
Submitted (02-DEC-1998) Center for Cancer Resea
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AF110194
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GINCLHQNPLSQVCIGVG"
1 245 c 235 g 242 t
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/allele="UGT1A1*33"
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/db_xref="taxon:9606"
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                              Tran, H.M., Kimura, S.,
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                                                                                                   Mammaila; Eutherla; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2351)

Ritter,J.K., Crawford,J.M. and Owens,I.S.

Cloning of two human liver billrubin UDP-glucuronosyltransferase cDNAs with expression in COS-1 cells
J. Biol. Chem. 266 (2), 1043-1047 (1991)
                                                                                                                                                                                                                                                                                                                                     complete cds.
M57899
M57899.1 GI:184472
                                                                                                                                                                                                                                                                                                                                                                                              HUMHUGBR1 2351 bp mRNA PKI U/-MAK-12
Human bilirubin UDP-glucuronosyltransferase isozyme 1 mRNA,
                                                                                          91093210
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                        UDP-glucuronosyltransferase; bilirubin UDP-glucuronosyltransferase Human adult female liver, cDNA to mRNA, clones Z6, Z11 and Z6MB2.
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92147680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%; Score 21; DB 97;
Similarity 100.0%; Pred. No. 0.74;
21; Conservative 0; Mismatches 0;
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                                             Location/Qualifiers
1. .2351
/organism="Homo sapiens"
/isolate="AK"
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QNFLCDVVXSPYATLASEFLQREVTVQDULSSASVWLFRSDFVKDYPRPIMPNMVFVG
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GAIQQLQQRGHEIVVLAPDASLYIRDGAFYTLKTYPVPFQREDVKESFVSLGHNVFEN
DSFLQRVLKTYKKIKKDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSFIV
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32...4
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/note="does not fit consensus"
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/protein_id="AAA61248.1"
/db_xref="GI:340132"
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/tissue_lib="cosmid"
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                                                                                         UDP-glucuronosyltransferase gene
                                                                                                                                                                                                                                 bilirubin UDP-glucuronosyltransferase 1. Homo sapiens DNA.
                                                                                                                                                                                                                                                                                             D87674 3341 bp DNA PRI 14-APR-2000 Homo sapiens gene for bilirubin UDP-glucuronosyltransferase 1 promoter region and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100
21; Conservative
                                                                                                                               Ueyama, H., Koiwai, O., Soeda, Y., Sato, H., Satoh, Y., Ohkubo, I. and
Doida, Y.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                       hnalysis of the promoter of human bilirubin
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                                         (bases
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                                                        Res. 9, 152-163 (1997)
                                         1 to 3341)
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/db_xref="Gi:184473"
/db_xref="Gi:184473"
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/note="G00-120-007"
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76. .1614
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GINCLHQNPLSQEFBAYINASGEHGIVVFSLGSMVSEIPEKKAMAIADALGKIPQTVL
WRYTGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGYYESICNGVPMVMMP
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/clone="26"
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sozyme 1"
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/sex="female"
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3 (bases 1 to 68770)

Waterston, R.H.

Direct Submission
Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 68770)
                                                                                                                                                                   Gattung, S., Stoneking, T. and Davidson, T. The sequence of Homo sapiens BAC clone RP11-154L24
                                                                                                                                                                                                                                                Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 68770)
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AC006985.2 GI:5732165
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Homo sapiens BAC clone RP11-154L24 from
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3101, 3112
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/db_xref="taxon:9606"
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/protein_id="BAA25600.1"
/db_xref="GI:3059177"
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repeat_;	FEATURES Source						JOURNAL	REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE JOURNAL	TITLE JOURNAL
/clone_lib="RPCI-11" /clone_3. 192 /rpt_family="L1" region 221528	The clone RP11-154L24 contains a tandem repeat from base positions 38234 to 39039, this region contains some low quality data. The assembly is consistent with the restriction digest information. Location/Qualifiers 168770 /Organism="Homo sapiens" //bb_xref="raxon:9606" //chromosome="2" //clone="RP11-164124"	SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An Improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com) or Pieter de Jong (http://bcpac.med.buffalo.edu) VECTOR: pBACe3.6 MEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-332L11, 200 bp overlap. Actual start of this clone is at base position 86134 of RP11-154L24.	MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. Mapping information for denetics, Washington University, St. Louis MCPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.	NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.	Center: Washington University Genome Sequencing Center Center code: WUGSC  Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu  Center project name: H_NH0154L24	ted (21-DEC-199) sity, 4444 Fore, 13, 1999 this;	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 6 (bases 1 to 68770) Waterston, R. Direct Submission	Department of Genetics, Washingto	Waterston,R.H. The Management of Management Submission Submitted (13-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

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/rpt_family-"L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                       Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, I., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Menga, V., Morrow, J., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisrani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                           Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Plerre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Illev,I., Johnson,R., Johnson, Kana,L., Kara
Flowland,J.C., Illev,I., Johnson,R., Johnson, Kana, L., Kara
Flowland,J.C., Illev,I., Johnson, R., Johnson, Kana, L., Kara
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Colkingalter, B., Choepel, Y., Colangelo, M., Collins, S., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collins, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 176619)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 11, clone RP11-689A10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%; score 21; DB 86; Length 68770; Similarity 100.0%; Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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33835. .34127
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29276. .29434
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0. .35762
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Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13617 13716; gap of 100 bp 13717 16173; gap of 100 bp 16074 16173; gap of 100 bp 16074 16173; gap of 100 bp 16174 18510; contig of 2337 bp 18511 18610; gap of 100 bp 20496 20595; gap of 100 bp 20496 20595; gap of 100 bp 20596 23548; contig of 2953 bp 23549 23648; gap of 100 bp 23649 25910; contig of 2262 bp 25911 26010; gap of 100 bp 26011 28060; contig of 2360 bp 26011
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3999 4098: gap of 100 bp
4099 5777: contig of 1679 bp in le
5778 5877: gap of 100 bp
5878 7685: contig of 6770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L6277
Center clone name: 689_A_10
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48729 48828: gap of
48829 52099: contig of
52100 52199: gap of
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                                                                                                                                                                                                                                                           37697 37796:
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1434 2787: co
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                                                                                                                                                                                                                                                                                                                    51 28160: gap of 100 bp
30134: contid of 1974 bp
35 30234: gap of 100 bp
35 30234: gap of 2412 bp
47 32746: gap of 100 bp
47 35096: contid of 2350 bp
37 35196: gap of 100 bp
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                                                                                                                                 45618:
                                                                                                                                                        40639: gap of 100 bp
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                                                                                  618: gap of 100 bp 48728: contig of 3110 l
                                                                                                                                                                                            40539: contig of 2743
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9926: contig of 1650 bp in length
26: gap of 100 bp
11499: contig of 1473 bp in length
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8176: contig of
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3: gap of 100 bp
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contig of 1808 bp in length
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of 391 bp in length
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f 3271 bp in length
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64948 65047: gap of

168 74267:

78288: gap of 81664: con

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105885 105984: gap of 100 b
105985 111486: contig of 5502
111487 111586: gap of 100 b
111587 17781: contig of 6195
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90546 95008; contig of 4463 bp in length
95009 95108; gap of 100 bp
95109 100587; contig of 5479 bp in length
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56748 56847: gap of 100 bp 16848 60467: contig of 3620 bm 4- 10468 60567: gap of 3620 bm 4- 1568
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                                  note "assembly_fragment"
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125343; contig of 7462
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81664: contig of 3076 bp in length
81764: gap of 100 bp
85169: contig of 3405 bp in length
85269: gap of 100 bp
90445: contig of 5176 bp in length
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69531: gap of 100 bp
74167: contig of 4636 bp in length
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176619: contig of 12929 1
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132608: gap of 1005 b
141190: con-
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163590: contig of 10934
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52556: contig of 11266
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78188: contig of 3921 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF297093 198872 bp DNA PRI
HOMO Saplens UGT1 gene locus, complete sequence.
AF297093
AF297093.1 GI:11118740
                                                                                                                                                                                                                                                                                                       Submitted (10-AUG-2000) Heritable Disorders Branch, NIH-NICHD, 9000 Rockville Pike, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Owens, I.S., Gong, Q., Cho, J.W., Huang, T., Potter, C., Gholami, N., Basu, N.K., Kubota, S., Carvalho, S. and Pennington, M.W. Thirteen UDP glucuronosyltransferase genes encoded at the human
                                                                                                                                                                                                                                                                                                                                                         Owens, I.S., Gong, Q., Cho, J.W., Huang, T., Potter, C., Gholami, N., Basu, N.K., Kubota, S., Carvalho, S. and Pennington, M.W.
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l (bases 1 to 198872
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FSLPSYVFTRGIFCHHLEEGAQCPAPLSYVPNDLLGFSDAMTFKERVWNHIVHLEDHL
FCQYLFRNALEIASEILQTPYTAYDLYSHTSIWLLRTDFYLDYPKPVMPNMIFIGGIN
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FSQYFSKNALEIASEILGTPYTAYDLYSHTSIWLLETDFVLDYJRFVMNMIFIGGIN
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PLDLAVFWVEFYMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Julu(<53103. .53957,181788. .181919,182603. 
189974. .183193,187016. .>187313) 
7gene-"UGTIA10" 
7product "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGYRKCLGKKGRVKKAHKSKTH"
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TGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFG
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                                                                                                                                                                                                                                                                                                                                                                                  oin(64509. .65011,65353. .65608)
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1011(53103. 53957,181788. 181919,182603. 182690,

182974. 181393,187016. 187313)

gene-"UGT1A10"
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                                                                                                                                                                                                                                  /gene-"UGTIA5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPITAPOTEYNNMIVIGLYFINOGSLLQDBOTLMFFRSKEDALFGDALFGGVILA
EYLGFSVYLFRGPGSLBHTFSRSDPVSVIPRCYTKSDHMTFSQRAMELVNLLE
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TGTRESNLAANT ILYKWLOODLLEHMENAFITHAGSHGYVESICNGYPMYMPLIFG
DQMDAKAWETKAAGTTLNYLEMTSEDLENALKAY INDKSYKENIMRLSSLHKORPYE
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TGTRESHANNTILVKWLPONDLIGHPMTRAFITHGSHAVYE BICNOKYPMMPLFG
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LCHRFFKNALBIASBILGTPVTBYDLYSHTSIWLLKTDFVLDYPKPYMPNMIFIGGIN
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RSIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDPFDNCGLIVAKY
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KGYRKCLGKKGRVKKAHKSKTH*
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182974. .183193,187016. .>187313)
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AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-APR-2001) Drug Metabolism, Merck & Co. Drop RY80L-109, PO Box 2000, Rahway, NJ 07065, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dean,B.J., Zhao,S. and King,C.
Nucleotide and Deduced Amino Acid Sequence of a Novel
UDP-Glucuronosyltransferase 1A Isoform Cloned from Male Rhesus
Monkey Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rhesus monkey.
Macaca mulatta
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Dean, B.J., Zhao, S. and King, C.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rect Submission
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lehligipavfelrnipcdldekgtqcpnbssylpehlltinsdhmtelqrvknmlyph
                                                                                                                                                                                                                                                                                                                                                                                                               'sex="male"
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Pred. No. 0.83;
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HOMO SAPIENS Chromosome 16q24.3 clone RP4-754F23,
SEQUENCE, 35 ordered pieces.
ACO7905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-NOV-1998) Molecular Endocrinology, Laval University, 2705 Laurier Boulevard, Sainte-Foy, Que GIV462, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis
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Albert, C., Vallee, M., Beaudry, G., Belanger, A. and Hum, D.W.
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Kremmidiotis, G., Gardner, A.E., Callen, D.F. and Sutherland, G.R
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AQYLSLPTVETLNALPCSLESEKTQCPNPETSYVERELSAHSDHMFTELQRVKNMLTAFS
QNELCOVVYSEYATLASSEFURENTVQNLLSSASVMLLSSDEVKDYPRPIMPNMAFIG
GINCLHQSPLSQEFEAY INASGEHGIVVFSLGSMYABIPEKKAMAIADALGKIPQTVL
WRYTGTPPSHLANNTILVKMLPQNDLLGHPMTRAFITHAGSHGIYEGICNGVPMYMMP
LFGDQNDNAKRMETKGAGYTLNVLEMTSEDLENALKAVINDKSYKENIMHLSSLHKOR
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/protein_id-"AAF15549.1"
/protein_id-"AAF15549.1"
/db_xref-"G1:6537144"
/translation-"MAVESGGRHPLVLGLLLCVLGPVLCHAGKNLLIPVDGSHWLSML
/translation-"MAVESGGRHPLVLGLLLCVLGPVLCHAGKNLLIPVDGSHWLSML
GTIQQLQQRGHEIVYLAPDASLLIREGAFYTLKTYPVPQREDYKESFVSLGHNVEN
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/db_xref="taxon:9541"
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1. .1647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently
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1 1479: contig of 1479 bp in length
1480 1487: gap of unknown length
1488 6699: contig of 5212 bp in length
6708 6707: gap of unknown length
6708 10905: contig of 4198 bp in length
10916 10912: gap of unknown length
10917 10918: contig of 821 bp in length
10918 10918: contig of 821 bp in length
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                                                                                                                                                                                                                                                                                                                                                 2: gap of unknown length
2: contig of 1710 bp in length
3: gap of unknown length
3: contig of 1774 bp in length
3: contig of 1774 bp in length
3: gap of unknown length
4: contig of 698 bp in length
5: gap of unknown length
6: contig of 4819 bp in length
6: gap of unknown length
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0: contig of 1971 bp in length
7: gap of unknown length
0: contig of 933 bp in length
7: gap of unknown length
9: contig of 4412 bp in length
6: gap of unknown length
6: gap of unknown length
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                            g of 307 bp in length if unknown length length g of 660 bp in length it unknown length g of 7839 bp in length if unknown length
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lg of 4819 bp in length
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ig of 2632 bp in length
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                                                                                                                                   on Jun 4, 2000 this sequence version replaced g1:8018160. During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known that the contract contracts of the contract of the contra
                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                            annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSDJ137K2 187507 bp DNA PRI 24-JUL-2000 Human DNA sequence from clone RP1-137K2 on chromosome 6q25.1-25.3. Contains part of the gene for a novel protein similar to B120 (contains KIAA1235), ESTs, STSs, GSSs and two putative CpG islands,
                                                                             feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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- 1	note-"MIR repeat: matches 14219 of consensus"	1	repeat_region 15034. 15291		/note≂*Alu repeat; matches 249302 of consensus" repeat region 14677. 14870		GSS: Em:AO312897"	/note="	/note="Alusg repeat: matches 1280 o	Alusg/x repeat: matches 80:	131 151 151 151 151	sies 2 mer tt 82% conserved"	'n	/note-	/note="AluJo repeat: matches 132302 of consensus" repeat_region 10795, .10905	peat: matches 2080, ,241/ c	10165	99699 te="12 reseat: matches 25792708 of	repeat_region /589 .7889 /note="AluSx repeat: matches 1 .305 of consensus"	/note=	/note- 7142	/note="AluJ/FLAM repeat: matches 166 of consensus" repeat_region 67687057	speat: matches 20/12/41 O	epear: marches 15: .100 of co	repeat: matched 15 153 of	repeat_region 51085417 /note="Alux repeat: matches 1297 of consensus"	complement(3848432 /note="match: GSS: Em	no/	/note="	מאוודה	/clone_lib="RPCI-1" repeat_region 1, 230	/map="q25.1-25.3" /clone="ap1-137K"	/db_xref="taxon:9606" /chromosome="6"	source 1. 187507 /organism="Homo sapiens"	right end of clone Rp1-80E10 is at 27741 in this sequence.	sequen	see http://bacpac.med.buffalo.edu/	RP1-137K2 is from the library RPCI-1 constructed at the Roswell	tion can be found at /HGP/Chr6	some 6, constructed 1		on the WORMPEP database can be found at		Wed Jul 25 10:29:00 2001 us-09-142-095-2.rge
/note=	/note="MLTIH repeat: matches 5/504 or consensus	.37354	repeat_region 3552735791 /note="%L2 repeat; matches 21592428 of consensus"	/note="I	OHSET AV	n •	<pre>misc_feature complement(3366834018)     /note="match: STS: Em:G24299"</pre>		/note="AluSx repeat: matches 129/ of consensus repeat region 3358133709		.32813	repeat_region 3137531688 /note="AluSx repeat: matches 1308 of consensus"	/note="	/note="		֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	29118	a".	/note="match: GSS: Em:	/note="match: GSS:	/evidence=not_experlmental misc_feature 27853, 28381	misc_feature 2782229153 /note="CpG island"	/note="MIR r		region	1291 of	: GSS: EM:AQ000/01		72 - Fm. AO526363 *	<pre>19</pre>	6 repeat: matches 1	repeat_region 2324123349 /note="MER33 repeat: matches 34142 of consensus"	repeat_region 2212722450 /note="L2 repeat: matches 15791915 of consensus"	compleme /note-"m	n 19765. 20073	/note-"}	/note	/note% copies o mer tigit s/s conserved	17556	17564	repeat_region 17234. 17514 // note-"Aluso repeat: matches 1283 of consensus"	/note-"4 copies 13 mer 84% conserved"		《《《··································

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Query Match 84.8%; Score 17.8; DB 93; Length 187507; Best Local Similarity 90.5%; Pred. No. 53; Matches 19; Conservative 0; Mismatches 2; Indels 0;
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// note="12 repeat: matches 2009. .2202 of consensus"
// note="2 copies 66 mer 96% conserved"
// 14505. .46069
// note="Aluxb repeat: matches 1 .294 of consensus"
// 16214. .46442
// note="Aluxb repeat: matches 83 .311 of consensus"
// note="Aluxb repeat: matches 83 .311 of consensus"
// note="6 copies 59 mer 70% conserved"
// note="6 copies 59 mer 70% conserved"
// 16520. .46747
// note="3 copies 66 mer 74% conserved"
// 16520. .46825
// note="19 copies 13 mer 66% conserved"
// 16520. .46830
// note="19 copies 13 mer 61% conserved"
// 16830. .46830
// note="29 copies 13 mer 61% conserved"
// 16845. .46830
// note="29 copies 2 mer tc 87% conserved"
// 16845. .46810
// note="19 copies 2 mer tc 87% conserved"
// 16845. .46830
// note="19 copies 2 mer tc 87% conserved"
// 16845. .46830
// 16845. .47132
// note="19 copies 2 mer tc 87% conserved"
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Search completed: July 25, 2001, 05:16:58 Job time: 9221 sec

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## SUMMARIES

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                                                                   /organism="unidentified"
/db_xref="taxon:32644"
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AF135471 208 bp DNA PRI 21-NOV-1999 saimiri boliviensis UDP-glucuronosyltransferase IA1 (UGTIA1) c promoter region and partial cds.
AF135471
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Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L.
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
variability at the uridine diphosphate glucuronosyltransferase 1A1 promoter in human populations and primates pharmacogenetics (1999) In press
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 234)
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Similarity 100.0%;
21; Conservative 0;
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                                                                             Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
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/product_"UDP-glucuronosyltransferase
/protecln_id="AAF09182.1"
/db_xref="GI:6456560"
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/db_xref="taxon:27679"
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/gene="UGT1A1"
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Ybazeta, G., Hall, D. and Di Rienzo, A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pharmacogenetics (1999) In press
2 (bases 1 to 234)
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/protein_id="AAF09173.1"
/db_xref="GI:6456542"
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/db_xref="taxon:9597"
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/db_xref="taxon:9598"
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                             /codon_start=1
/product="UDP-glucuronosyltransferase lAl"
/protein_id="AAF09174.1"
/db_xref="GI:6456544"
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                                                                                                                                            'product="UDP-glucuronosyltransferase lAl"
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Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laboratory, Medical Submitted (63-FEB-2001) Medicine/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA Location/Qualifiers
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1 (bases 1 to 531)

McKle,K., Kutlar,F., Glendenning,M. and Kutlar,A.

MCKle,K., A
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McKie, K., Kutlar, F., Glendenning, M. and Kutlar, A.
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/db_xref="G1:13569709"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-AUG-1999) Medicine, Hematology/Oncology-Sickle Cell Center, Medical College of Georgia, 15th Street, AC-1000, Augusta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kutlar,F., Sromek,E., Leithner,C., Nechtman,J. and Kutlar,A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with sickle cell anemia
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Direct Submission
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                             /db_xref="GI:601050"
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
GAIQQLQQRGHEIVYLAPDASLXIRDG"
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                                                                                                        /gene="UGT1"
/note="UDP glycosyltransferase
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A65504
                                            Submitted (04-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hisao Ueyama, Shiga University of Medical Science, Department of Medical Biochemistry; Seta, Otsu, Shiga 520-21, Japan (Tel:077-548-2162,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV DUNDEE (GB)
Other publication AU 2224197 19970916.
Sequence updated (08-Jan-1997)
Location/Qualifiers
                                                                                                                                                                                                             Ueyama, H., Koiwai, O., Soeda, Y., Sato, H., Satoh, Y., Ohkubo, I.
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 9732042-A 5 04-SEP-1997;
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2 (bases 1 to 3341)
                                                                                                                                                                       Analysis of the promoter of human bilirubin UDP-glucuronosyltransferase gene (UGT1*1) in
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/db_xref="taxon:32644"
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Homo sapiens BAC clone
AC006985
AC006985.2 GI:5732165
Waterston, R.
Direct Submission
                         MO 63108, USA
5 (bases 1 to 68770)
                                                        Submitted (13-AUG-1999). Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                    Waterston, R.H
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                                                                                                                                               Direct Submission
Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                        Gattung, S., Stoneking, T. and Davidson, T. The sequence of Homo sapiens BAC clone F
                                                                                                                                                                                                                                                                                                  Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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/product="bilirubin UDP-glucuronosyltransferase 1"
/protein_id="BAA25600.1"
/db_xref="GI:3059177"
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/db_xref="taxon:9606"
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                                                                                                                                                                    Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, on Aug 13, 1999 this sequence version replaced g1:4337256.
                                                                                                                                                                                                                                                                                                                                Submitted (22-OCT-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 68770)
                                                                                                                                                                                                                                                                                  Direct Submission
                            Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
Center project name: H_NH0154L24
                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
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COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc MAPPING INFORMATION:

The clone sequenced to the left is RP11-332L11, 200 bp overlap. Actual start of this clone is at base position 86134 of RP11-332L11; actual end is at base position 68770 of RP11-154L2 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male NEIGHBORING SEQUENCE INFORMATION: http://bacpac.med.buffalo.edu) OI RP11-154L24.

FEATURES repeat\_region repeat\_region source repeat\_region repeat\_region The clone RP11-154124 contains a tandem repeat from base positions 38234 to 39039, this region contains some low quality data. The assembly is consistent with the restriction digest information. Location/Qualifiers /rpt\_family-"Alu" 529. .1634 /rpt\_family="L1" 221. .528 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="2" /rpt\_family="Ll" 1658. .1878 /clone="RP11-154L24" /clone\_lib="RPCI-11" /map="2" .68770 \_family-"MIR"

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  Direct Submission Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                  Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKerman, K., Mcheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKerman, K., Mcheeters, R., McCarthy, M., Maylor, J., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tralamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC026497 176619 bp DNA HTG 22-MAR-2000 HOMO Sapiens chromosome 11 clone RP11-689A10 map 11, *** SEQUENCING IN PROGRESS ***, 43 unordered pieces.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-689A10
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                                                                                                          Coung,G., Zainoun,J., Zimmer,A. and Zody,M.
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3. .12523

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NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                         Center project name: L6277
Center clone name: 689_A_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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1433: gap of 100 bp
2787: contig of 1354 bp in length
2887: gap of 100 bp
3998: contig of 1111 bp in length
4098: gap of 100 bp
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18510: contig of
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10539: contig of 2743 bp in length
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96: contig of 2500 bp in length
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85170 85269: gap of 5176 bp in length
90445 90545: gap of 100 bp
20546 90545: gap of 4463 bp in length
100 bp
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'clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
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8188: contig of 3921
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Homo sapiens UGT1
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AF297093.1 GI:11118740
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Owens, I.S., Gong, Q., Cho, J.W., Huang, T., Potter, C., G
Basu, N.K., Kubota, S., Carvalho, S. and Pennington, M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198872).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-AUG-2000) Heritable Disorders Branch, NIH-NICHD, 9000 Rockville Pike, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UGT1 locus
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20105. .20956
/gene="UGT1A11p"
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45619. .48728
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17797. .40539
oin(<34264. .35118,181788. .181919,182603. .182690
                         34133. .>187313
'gene="UGT1A8"
                                                                /gene="UGT1A8"
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ob_xref="taxon:9606"
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"gene-"UGT1A11p"
"note-"UDP glucuronosyltransferase 1A11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="UGT1A12p"
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VEKLILRGHEYVVYMPEVSWQLGKSLNCTVKTYSTSYTLEDLDMEFMDFADAGWKAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MARAGWTSPVPLCVCLLLTCGFAEAGKLLVVPMDGSHWETMQSV
VEKLILRGHEVVVVMPEVSWQLERSLKOTVKTYSTSYTLEDQNREEMVFAHAQWKAQA
VEKLILRGHEVVVVMPEVSWQLERSLKOTVKTYSTSYTLEDQNREEMVFAHAQWKAQA
QSIFSILMSSSSGFLDLFFSHCRSLFNDKKLVEYLKESSFDAMTFKERVWHNIVHLEDHL
FCQYLFRNALEIASEILQTFVTAYDLYSHTSIWLLRTDFVLDYFXDWHNWHIVHLEDHL
FCQYLFRNALEIASEILQTFVTAYDLYSHTSIWLLRTDFVLDYFXHWNIVHLEDHL
FCQYLFRNALEIASEILQTFVTAYDLYSHTSIWSHAHAIADALGKIFQTVVMRY
CHQGKFLPMEFEAYINASGEHGIVVFSLGSWYSEIFEXKAMAIADALGKIFQTVVMRY
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52972. .>187313
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join(34264. .35118,181788. .181919,182603.
182974. .183193,187016. .187313)
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/gene-"UGT1A9"
88416. .88427
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join(53103. .53957,181788. .181919,182603. .182690,

182974. .183193,187016. .187313)

'gene="UGT1A10"
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DQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
PLDLAVEWVEFYMRHIGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
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/gene="UGT1A8"
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CHQGKPLPMEFEAYINASGEHGIVVFSLGSMVSEIPEKKAMAIADALGKIPQTVLMRY
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                                                                     /product-"UDP glucuronosyltransferase 1A9"
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/translation-"MACTGMTSPLPLCVCLLLTCGFAEAGKLLVVPMDGSHWFTMRSV
VEKLILRGHEVVVYMPEVSWQLGRSLNCTVKTYSTSYTLEDLDREFKAFAAAGWKAQV
VEKLILRGHEVVVYMPEVSWQLGRSLNCTVKTYSTSYTLEDLDREFKAFAAAGWKAQV
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182974. .183193,187016. .>187313)
/gene="UGT1A10"
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      LCHRFFKNALEIASEILQTPVTEYDLYSHTSIWLLRTDFVLDYPKPVMPNMIFIGGIN
                           RSIYSLLMGSYNDIFDLFFSNCRSLFKDKKLVEYLKESSFDAVFLDFFDNCGLIVAKY
FSLPSVVFARGILCHYLEEGAQCPAPLSYVPRILLGFSDAMTFKERVRNHIMHLEEHL
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join(88543. 89397,181788. .181919,182603.
182974. .183193,187016. .187313)
'gene-"UGT1A9"
                                                                                                                                                                                                                                                                                            join(<88543. .89397,181788. .1819
[82974. .183193,187016. .>187313)
/gene "UGT1A9"
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'gene="UGT1A13p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"UDP glucuronosyltransferase 1A13"
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182974. .183193,187016. .>187313) 
/gene-*UGTIA/*
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TGTRPSKLANNTILVKKLPONDLLGHPMTRAFITHAGSHCVYESICNOKOPMYMAPLFG
DOMUNAKBAETKGAGVTLMVLEMYSEDLENALKAVINDKSYKENIMELSSLHKDREPVE
PLDLAVFMVEFVMRHKGAPHLRPAAHDLTMYQYHSLDVIGFLLAVVLTVAFITFKCCA
/tianslation="matglqvplpqlatglilllgvqppaasgkvlvvptdgshhlsn
realrdlharghqvvvltlevnnyikeenfftlttyaismtqdefdrlilghtqsfff
tehllatsgrvaindhenlsh
                                                                                                                                                                                                                                                                                                                      JULIN (<129500. .130465,181788. .181919,182603. .182690,
182974. .183193,187016. .>187313)
7genem (GGTA5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SELTAPQTEYRNNMIVIGLYFINCOSLLQDRDTLNFFKESKFDALFTDPALPCGVILA
EYLGLPSVYLFRGFPCSLEHTFSRSPDPVSYIPRCYTKFSDHWTFSQRVANFLYNLLE
PYLFYCLFSKYEELASAVLKRDVDIITLYQKYSVALLRUDFVLEYPRPVMPNMVFIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTRPSNLANNTILYKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMYMMPLFG
DQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
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FSLPSVVFARGIFCHYLEEGAQCPAPLSYVPRLLLGFSDAMTFKERVKNHIMHLEEHL
FCPYFFKNVLEIASEILQTPVTAYDLYSHTSIWLLRTDFVLEYFKPVMPNMIFIGGIN
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join(98552. .99406,181788. .181919,182603. .182690
182974. .183193,187016. .187313)
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/gene="UGT1A7"
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129525.
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/protein_id="AAG30420.1"
/db_xref="GI:11118745"
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182974. .183193,187016. .≻187313)
∕gene≖"UGTIA6"
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VEKLILRGHEVVVVAPEVSWQLGRSLNCIVKIYSTSYTLEDQDREFMVFADARWIAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="UDP glucuronosyltransferase 1A7'
/protein_id="AAG30419.1"
/db_xref="GI:11118744"
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                                                                                     /product="UDP glucuronosyltransferase 1A5"
/protein_id="AAG30421.1"
/db_xref="GI:11118746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAYGYRKCLGKKGRVKKAHKSKTH*
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IVEVLSDRGHEIVVVVPEVNLLLKESKYYTRKIYPVPYDQEELKNRYQSFGNNHFAER
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)oin(109610. .110470,181788. .181919,182603. .182690,
182974. .183133,187016. .187313)
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/gene="UGT1A6"
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                                                                                                                                                                                                                    'gene="UGT1A5"
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oin(129600. 130466,181788. 181919,182603. 182690,
82974. 183133,187016. 187313)
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

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                                                                                                                      Submitted (07-0CT-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6; On Apr 4, 2000 this sequence version replaced gi:5870295.
                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (07-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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Submitted (31-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                    MO 63108, USA
5 (bases 1 to 136868)
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Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens BAC clone RP11-422A6 from 2, complete sequence.
                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                     MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Web site: http://genome.wustl.edu/gsc
contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0422A06
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                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
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ALSYLCHAVSAPYASLASELFQREVSVVDLVSHASVWLFRGDFVMDYPRPIMPNMVFI
GGINCANGKPLSQEFEAYINASGEHGIVVFSLGSWYSEIPEKKAMAIADALGKIPQTV
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PLFGDQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKD
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanses, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is RP11-32P22, 200 bp overlap; the clone sequenced to the right is RP11-122E16. Actual start of this clone is at base position 149634 of RP11-32P22; actual end is at base position 136868 of RP11-422A6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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FEATURES

Location/Qualifiers

'db\_xref="taxon:9606" 'chromosome="2" organism="Homo sapiens"

clone\_lib="RPCI-11"

Lone-"RP11-422A6"

rpt\_family-"L2"

\_family-"Retroviral"

\_family="(TAAA)n"

\_family="Retroviral"

\_family-"L2"

NEIGHBORING SEQUENCE INFORMATION:

(http://bacpac.med.buffalo.edu)

pBACe3,

SOURCE INFORMATION:

MAPPING INFORMATION: restriction digest.

source

repeat\_region repeat\_region repeat\_region misc\_feature

rpt\_family-"L2"

rpt\_family-"Alu"

rpt\_tam

11y-"L2"

note- match to EST

repeat\_region repeat\_region repeat\_region repeat\_region

\_family-"Ll"

\_family-"Alu"

\_family="Alu"

y-"L1"

repeat\_region repeat\_region

family-"GA-rich"

y-"L1"

family-"L2" family-"MaLR"

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

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ACCESSION
VERSION
KEYWORDS
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                       Eukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                            1 Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
The sequence is a part of the data (ACCESSION NO. AP000174 -
                                               Homo sapiens
                                                                            AC087204.1 GI:11693386
HTG; HTGS_PHASEO.
                                                                                                                            SAMPLING
                                                                                                                                            Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone;020D3, complete sequence.
                                                                                                                                                           AC087204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP000194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (6SC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Homo sapiens 7,218bp genomic DNA of 21q22.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7218)
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/db_xref="taxon:9606"
/chromosome="21"
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                                                                                                                                          B clone RP11-520F7 map 8,
                                                                                                                                                                                                                                                                                                            M1smatches
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Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
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Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
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Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Romen, J., Rosetti, M.,
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Sougnez, C., Spencer, B., Stange-Thomann, N., Tscfaye, S., Theodore, J.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
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Wallson, B., Wallson, J., Wallson,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiess chromosome %, clone RP11-520F7
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Smit, A.F.A. & Green, P. (1996-1997)
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Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Lehoczky, J., Levine, R., Lehoczky, Lehoczky, J., Levine, R., Lehoczky, Lehoczky, Lehoczky, R., Lehoc
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                                         On Feb 27, 2001 this sequence version replaced gi:12831877. On Feb 27, 2001 this sequence version replaced gi:12831877. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
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[] (bases 1 to 47972)
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                                                                                                                                                                                                                                                                                                                                                  Submitted (22-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire
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         corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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43064 43713: contig of 650 bp tr
43714 43813: gap of 100 bp
43814 44501: contig of 688 bp tr
44502 44601: gap of 100 bp
44602 45262: contig of 661 bp tr
45263 45362: gap of 100 bp
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/db_xref = "taxon: 9606"
/chromosome = "8"
/map = "8"
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/clone_lib="RPCI-11
8764 c 9356 g
                                                                                                                                                                                                                                                                                                             UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Pred. No. 40;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone RP11-592B10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-411F9 is at 47873 in this sequence true right end of clone RP5-1007B16 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584. .673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER61E repeat: matches 377. .477 of consensus"
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complement(156. .512)
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/db_xref="taxon:9606"
             note="L1M3 repeat: matches 3546, .5738 of consensus"
                                                                                                                                                                                                                                                                                        /note="single clone region. Assembly confirmed by
restriction digest data."
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                                                                                                                                  note-"L1M3 repeat: matches 2143, .. 3546 of consensus"
                                                                                                                                                                                                                                   note-"AluY repeat; matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                              344. .7825 note="LIR22 repeat: matches 1. .509 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LTR30 repeat: matches 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="LTR12 repeat: matches 189.
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                                                                                      note="Alusx repeat: matches 2. .308 of consensus"
                                                                                                                                                                                    note="LIMA1 repeat: matches 4254, .6304 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="HERVK22 repeat: matches 100. .6836 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR12 repeat: matches 582. .671 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                      ote="L1MA1 repeat: matches 685. .4254 of consensus"
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/note="ITR9 repeat: matches 6. .625 of consensus"
20213. .20397
/note="TilM4 repeat: matches 4454. .4646 of consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="T1gger2a repeat: matches 23. .433 of consensus"
19408. .20039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(25299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (25297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(24422.
                                                                                                                  /note="26 copies 2 mer at 84% conserved" complement(39249. .40015) /note="match: GSS: Em:AQ538237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(25327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"match: GSS: Em:AQ545471"
complement(25299. .25496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(25273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(28723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28722. .28935
/note-"AluY repeat: matches 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-*match: GSS: Em:B56335*
26210. .26253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2692.
complement(25273, .25508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"match: GSS: Em:AQ030189"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"MER77 repeat: matches 13.
                     'Aote="MIR repeat: matches 1. .259 of consensus" 10581. .40676
                                                                          /note-*match: GSS: Em:AQ171081*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"LTR15 repeat: matches 1. .489 of consensus" 17870. .27942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="MER90 repeat: matches 222. .543 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"match: GSS: Em:AQ902789"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="22 copies 2 mer tg 95% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match: GSS: Em:AQ376698"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ote-"MSTA repeat: matches 1.
                                                                                                                                                                                                                                            ote-"FLAM_A repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                            .3532
.e="31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e-"MLT1J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e-"AluY repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                         e-"MLTlAl repeat: matches 1. .210 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-"match: GSS: Em:AQ882343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- MER90 repeat: matches 543. .615 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - match: GSS: Em: AQ668040*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "MLT1J repeat: matches 117. .513 of consensus" .35066
                                                                                                   .40482
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                                                                                                                                                                                   .3839
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copies 2 mer aa 64% conserved"
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                                                                                                                                                                                                      copies 2 mer aa 67% conserved*
                                                                                                                                                                                                                                                                                                                                                                                                           copies 2 mer aa 80% conserved*
                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS: Em:AQ610704"
$40. .24857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .374 of consensus"
                                                                                                                                                                                                                                                 .124 of
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Search completed: July 25, 2001, 05:16:42 Job time: 9205 sec
                                                                                                                                                                                                                                                                                   BASE COUNT 16896 a ORIGIN
                                                                                                                                                                              Ouery Match 84.8%; Score 17.8; DB 90; Best Local Similarity 90.5%; Pred. No. 40; Matches 19; Conservative 0; Mismatches 2;
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/note="LIN2 repeat: matches -676. .-231 of consensus"
42139. .42439
/note="LIPA15-16 repeat: matches -265. .24 of consensus"
43901. .4364
/note="LiPA13 repeat: matches 802. .1288 of consensus"
43465. .43687
                                                                                                                                                                                                                                                                                                                                                                               /note-"MLT2B repeat: matches 1. .304 of consensus" complement(47070, .47394) /note-"match: GSS: Em:AQ053386" complement(47357. 47846) /note-"match: GSS: Em:AQ534016" 47878. .47972
                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ551896"
8982 c 8503 g 13591 t
                                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ186789" 47880. .47972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1PA16 repeat: matches 3178. .6153 of consensus"
46921, .47311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"LIPAL3 repeat: matches 1288. .1351 of consensus" 3755. .46738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="MER30 repeat: matches 1. ,230 of consensus"
8. ,43754
                                                                                                                                                                                                                      Length 47972;
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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21
1 aagtgaactccctgctacctt 21
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Listing first 45 summaries
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/SIDSI/gcgdata/geneseq/geneseqn/NA2000.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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                   18 AAT79541
19 AAT79540
19 AAV57903
21 AAC25716
21 AAC38612
21 AAA46500
20 AAX09252
22 AAF30011
16 AAO9786580
18 AAO97853
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                                                                                                                                                                                                                                                                                                            SUMMARIES
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Human secreted pro
Arabidopsis thalia
cDNA encoding enzy
Human CARD-4 DNA,
Human CARD-4 gene,
TROMPI DNA, Trepo
Treponema pallidum
Eucalyptus grandis
                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                              Upstream
                                                                                                                                                                                                          UGT1*1 gene
                                                                                                                                                                             Hereditary
                                                                                                                                                                                          Pene exon 1
                                                                                                                                                                             haemoch
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AAA48654 AAF75126 AAC76910	AAX78137 AAA73552	AAX99340	AAT61894	AAT34655	AAZ20051 AAZ20035	AAZ20052	AAZ20026	AA230444	AAT42133	AAT20482	AAC26942	AAC98243	AAX20500	AAV57926	AAT97955	AAC81899	AAV99562	AAC81718	AAC39039	AAC46144	AAZ98118	AAC77765	42	AAV04426
Human C'rai DNA, Human C'Raf CDNA, Human ORFX ORF2465	c-Raf- ucleoti	Human c-raf sequen	Human raf-1 cDNA.	s-associated	. Human rad17 cell c	cell	rad17 cell		Ascorbate-free-rad	Human gene signatu	Human secreted pro	Human colon cancer	Polynucleotide seg	Hereditary haemoch		ana SRp		6	dopsis	_	Human signal pepti	cancer asso	calpain	Human calpain smal

## ALIGNMENTS

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RESULT
AAT79541
    16-MAR-1996;
01-MAR-1996;
                                                                                                                                                                                                                    Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler Najjar; type 2; drug m
                                                                                                                                                                                                                                                              UGT1*1 gene exon 1 upstream PCR primer A.
Improving drug trial efficiency comprises identifying participants
                    WPI; 1997-448702/41.
                                          Burchell B;
                                                                                                                 03-MAR-1997;
                                                                                                                                      04-SEP-1997.
                                                                                                                                                                                                        Drug trial efficiency; screening; PCR primer;
                                                                                                                                                                                                                                                                                                       AAT79541;
                                                                                                                                                                                                                                                                                                                          AAT79541 standard; DNA; 21
                                                                                                                                                         WO9732042-A2
                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                  23-JAN-1998
                                                                                                                                                                              Homo sapiens.
                                                             UYDU-) UNIV DUNDEE.
                                                                                                                                                                                                                                                                                 (first entry)
                                                                                  96GB-0005598.
96GB-0004480.
                                                                                                                  97WO-GB00577.
                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                              Crīgier-Najjar; type 2; drug metabolism; eening; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                     Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler-Najjar; type 2; drug m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 12; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may hinder result interpretation
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                                           misc_feature
                                                                                                                                protein_bind
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                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          Drug trial efficiency; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Upstream DNA sequence of UGT1*1 gene exon 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 other;
                                                                                      protein_bind
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317..324
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/note= "feature indicated in patent, but no further
explanation is given"
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                                                                                                                                316..323
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/note= "feature indicated in patent, but
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Pred. No.
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1 aagtgaactccctgctacctt 21

Matches Query Match

Local

Similarity

100.0%;

Score 21; Pred. No.

0.21; DB 18; 0

Length 620; Indels

0

Gaps

0

Conservative

0,

Mismatches

Sequence 620 BP;

157

A; 127 C; 151 G; 185 T; 0 other;

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cc gene 1*1 excu 1. This gene is known to be associated to gene 1*1 excu 1. This gene is known form of unconjugated cc syndrome (GS). GS is a mild, common form of unconjugated cc syndrome (GS). GS is a mild, common form of unconjugated cc syndrome (GS). GS is a mild form the common form of the glucuronidation cc capacity, Analysis of the genetic basis of GS has allowed 2 forms to be identified. One is a mild form associated with homozygous 2 bp compared to the conterior of the GT1*1 excun 1, and cc mutation which, when homozygous, causes Crigier-Najjar type 2 disease. Cc The first form is aucosomal recessive and the second is inherited community. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an cc effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic cc basis of GS, and eliminated or included on basis of them possessing or of the UGT gene, using the primers described in AAT79541-44.
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999999
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with Gilbert's syndrome - useful as their altered drug metabolism
may hinder result interpretation
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01-MAR-1996;
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                                                                                                                                                                                                                                                             in the
                                                                                                                                                                                                                                                          sequence represents the upstream sequence, positions file patent, of uridine diphosphate glucuronosyltransferase
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96GB-0004480
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513..519
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syltransferase (UGT)
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Db 105327 aagtgaactcactgcaacct 105346
                                                                                                                                                                                                                                                                                                                                                           haemochromatosis (HFE) gene mutation in an individual comprising:

(C (a) providing DNA or RNA from the individual; and (b) assessing the
DNA or RNA for the presence or absence of a haplotype or genotype where

the presence or absence of the haplotype genotype indicates the likely
presence of the HFE gene mutation in the genome of the individual. The
HFE gene sequences from the present invention can be used to develop
products for use in the diagnosis and treatment of HFE. The present
invention also describes BTF genes, which are homologues of the milk
protein butyrophilin (BT), and can be used in the production of agonists
and antagonists of BT function. Also described are: (1) a Roket gene
which can be used to develop products for the study, diagnosis and
treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
thich are homologues of a type 1 sodium transport gene, and can
similarly be used for hypophosphatemia.
                                                                                                                                 Matches
                                                                                                                                                                        Query Match
Best Local
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Tsuchihashi Z, Wolff RK;
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01-OCT-1996;
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                                                                                                                                                                                                                                                                                              Sequence 237326 BP; 69596 A; 48904 C; 48217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (JHH) affected individual. Also described is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 9; 209pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism
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                                                                                                                                 18; Conservative
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                                                                                                                                 0; Mismatches
                                                                                                                                                                     Score 16.8;
Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                70609 T; 0 other;
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CL LAT. Buch

100 TEX 20 MONT

対数額

Arabidopsis thaliana DNA fragment SEQ ID NO: 21606:

17-OCT-2000 (first entry)

AAC38612;

RESULT 5

AAC38612 standard; DNA; 867

В

68 AAGGGAACTCGCTTCTACCTT 48 1 aagtgaactccctgctacctt 21 Conservative

Query Match
Best Local Similarity
Matches 18; Conserv

77.1%; 85.7%;

0;

Mismatches

Score 16.2; Pred. No. 46

46; DB 21; ω --

Length 260; Indels

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RESULT 4
AAC25716/c
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                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORR has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oliqo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein 5' EST, SEQ ID NO: 29791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-2000
Sequence 260 BP;
                                             expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 29791; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122487
  74 A; 58 C; 45 G; 82 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano
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### Action assay; genetic mapping; gene expression control; identification; signal transduction pathway;	principly gene expression control:  PR  PR  PR  PR  PR  PR  PR  PR  PR  P		9999999	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,,,,,,,	1999; 1999; 1999; 1999; 1999;	11-MAY-1999; 11-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999;	1999;	23-APR-1999; 23-APR-1999; 28-APR-1999; 30-APR-1999; 30-APR-1999;	99,	999999	25-FEB-2000; 20	EP1033405-A2.		Hybridisation a
apping; gene expression transduction pathway; semination sequence; ss.	principly gene expression control:  PR  PR  PR  PR  PR  PR  PR  PR  PR  P	99US-0139458 99US-0139460 99US-0139461 99US-0139461 99US-0139462 99US-0139763 99US-0139763 99US-0139763 99US-0139817 99US-0139817	9908-0139453 9908-0139492 9908-0139454 9908-0139455 9908-0139455 9908-0139457	99US-0137502. 99US-0137724. 99US-0138094. 99US-0138540. 99US-0138847. 99US-0139119. 99US-0139119.	99US-0136021. 99US-0136392. 99US-0136782. 99US-0137222. 99US-0137528.	99US-0134768. 99US-0134941. 99US-0135124. 99US-0135353. 99US-0135629.	ພ່ພພ່ພພ່ພ	in to in in i	908-013 908-013 908-013	99US-0128234. 99US-0128714. 99US-0129845. 99US-0130077. 99US-0130449.	905-011 905-011 905-011 905-011	00EP-0301439. 99US-0121825.		ay; promoter; liana.	ssay; genetic   ication; signa
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control;															( <b>5</b>
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JUN-1999 JUN	9908-0144 9908-0144	100000000000000000000000000000000000000	93684. 9175.	7416. 7493. 7935. 33171.	7038. 7204. 7302. 7192. 7260.	5919. 5386. 5388.	5218. 5224. 5913.	5085 5087 5192	1632. 1814. 1086.		331 331 331 331 331	5420.	8055. 8055.	84871.	ტ წ წ წ
JUL-1999 JUL	990S-014083 990S-014083 990S-014184 990S-014184 990S-014184 990S-014184 990S-014408 990S-014408 990S-014408 990S-014408 990S-014408 990S-014408 990S-014431 990S-014433 990S-014433 990S-014433 990S-014433 990S-014508 990S-014508 990S-014508 990S-014508 990S-014508 990S-014514 990S-014514 990S-014514 990S-014514 990S-014521 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014531 990S-014638 990S-014730 990S-	50654 50654													
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Best Local
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22-SEP-1999;
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16-SEP-1
                        Coffea arabica.
                                     Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase; ds
                                                  cDNA encoding enzyme involved in mannan polysaccharide hydrolysis.
                                                               04-SEP-2000
                                                                            AAA46500;
                                                                                         AAA46500 standard; cDNA; 1613
                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1999
29-SEP-1999
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                                                                                                                        678 AAGTGAACTCCTTGCGACTTT
                                                                                                                               1 aagtgaactccctgctacctt 21
                                                                                                                                                        Similarity
                                                                                                                                                  Conservative
                                                               (first entry)
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99US-0158029.
99US-0158232.
99US-0158369.
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0154039.
99US-0154779.
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99US-0157753
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             Location/Qualifiers
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3-0155659.
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85.78;
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160741.
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159331.
159637.
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Pred. No. 53;
0; Mismatches
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The present sequence encodes an endo-beta-mannanase enzyme, which is involved in the hydrolysis of polysaccharides that consist of molecules of mannan, either simple or branched, linked together by beta (1-4) bonds. The mannanase polysucleotide sequence is used for in vivo modification of the coffee endo-beta-mannanase gene. It is also used to produce transgenic plant cells (especially coffee cells) which have modified properties of mannan polysaccharide, and thus altered flavour or structure. The enzyme is used for modification, degradation or synthesis of mannan polysaccharides in vitro, particularly to treat coffee beans to increase the percentage of dry matter extraction, and thus reduce the quantity of sediment.
                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                  WPI; 2000-399535/34.
P-PSDB; AAY93441.
                                                                                                                                                                                                                                                                                                                                                                Marraccini P,
                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000.
Sequence 1613 BP;
                                                                                                                                                                                                                                                                    New DNA encoding endo-beta-mannanase from coffee, used e.g. in pharmaceutical, cosmetic or food compositions to hydrolyze polymannans
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                                                                                                                                                                                                                      29-30; 41pp; French.
                                                                                                                                                                                                                                                                                                                                                               Rogers J;
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520 A;
 305
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   347 G;
   441 T; 0 other;
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Ωy В Matches Ouery Match Best Local CARD-3; caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-45; CARD-45; CARD-47; Human CARD-4 DNA. 25-OCT-1999 AAZ09252; AAZ09252 standard; DNA; 32042 BP 408 AAGTGAACTCCATACTTCCTT 1 aagtgaactccctgctacctt 21 18; Similarity Conservative (first entry) 77.1%; 85.7%; 388 0 Score 16.2; Pred. No. 58; Mismatches DB 21;  $\omega$ Length Indels 1613; 0; Gaps 0;

1

10-03-765-133-

Key exon

Location/Qualifiers

Homo sapiens. CARD-42; human; ds.

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海南京人 不明確によるかい

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exon
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                 99WO-US02544.
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19834..21324
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6191..9024
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11182..11265
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cc assays, predictive medicine and therapeutic and prophylatic methods of treatment. The methods may be used to diagnose and treat patients which cc are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the FrsyApo-1 receptor complex, abnormal activity of the TNF receptor complex, or abnormal concerns a concern complex, or abnormal activity of the TNF receptor complex, or abnormal concerns complex, abnormal activity of the TNF receptor complex, or abnormal concerns con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and partial murine CARD-41 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-FEB-1998;
17-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 18; 181pp; English.
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98US-0099041.
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RESULT
AAF30011
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Best Local Similarity
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                                                                                       AAF30011;
                                                                                                   AAF30011 standard; cDNA; 32042 BP
                                                                                                                                       1 aagtgaactccctgctacctt
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                                                                                                                                                              77.1%;
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Pred. No. 83;
                                                                                                                                                          Mismatches
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Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other)

CARD-4; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; immune disease; inflammation; antitumour; antiseptic; immuneodulator; antiinflammatory; apoptosis; diagnosis;

23-APR-2001

(first entry)

Human CARD-4 gene.

gene therapy; chromosome 7; ds.

CDS

Location/Qualifiers 485..31768

Homo sapiens

exon

intron

exon

intron

exon

intron

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28-JUN-2000, 2000WO-US17691.
                28-JUN-1999; 99US-0340620.
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28033..31695
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9025..9108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of the human caspase recruitment commain 4 (CARD-4) gene on chromosome 7. CARD-4 exists in at least 4 forms, 1.e. the long form CARD-41 (see AAB20081), the short form CARD-42 (see AAB20081), and splice variants CARD-47 (see AAB20082) and CARD-42 (see AAB20082). It is an intracellular protein predicted to be involved in regulating caspase activation. It activates the NF-kappaB pathway and enhances caspase 9-mediated cell death. Methods of diagnosing and treating patients suffering cell death. Methods of diagnosing and treating patients suffering cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer viral infections, autoimmune diseases, neurological diseases and
                13-JUL-1995
                                          W. V. - 7598136.0M
                                                                                            mat_peptide
                                                                                                                                                                                                                                        TROMP1: rare outer membrane protein; Spirochaetaceae; immunogen; vaccine; syphilis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or polypeptide. Such disorders include cancer, wiral infection, autoimmune disorders, neurological diseases, haematological disorders. Inflammatory disorders and immune disorders. The CARD-gene is useful for genetic information and mapping and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 2001-061973/07.
P-PSDB: AAB20080, AAB20081, AAB20082, AAB20083.
                                                                                                                         sig_peptide
                                                                                                                                                                                                            Treponema pallidum subsp. pallidum.
                                                                                                                                                                                                                                                                                           TROMP1 DNA
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                                                                                                                                                                                                                                                                                                                                                           AAQ97865
                                                                                                                                                                                                                                                                                                                                                                                        AAQ97865 standard; DNA; 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 13; Fig 18; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations, e.g. mutations in splice donor or acceptor sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                /*tag- b
                                                                                                                                                                        Location/Qualifiers
                                                                               C-- CR3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2;
Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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Length 32042; Indels

Gaps

0;

The CARD-4

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04-JAN-2001.

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                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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06-JAN-1994;
07-JUN-1994;
                                                                                                                                                                                                                                         6580
P-PSDB; AAW22134
       WPI; 1997-393614/36
                    Blanco DR,
                                                                                                                              CDS
                                                                                                                                                               Rare; outer membrane protein; Treponema pallidum; Spirochaetales; Immune response; Syphilis; TROMP-1; precursor; ss.
                                                                                                                                                                                     Treponema pallidum rare outer membrane protein (TROMP-1) DNA
                                                                                                                                                                                                                                                                                                                                                    digest amino acid sequence analysis of EcoRI-digested genomic DNA of T. pallidum subsp. pallidum. It is the precursor of a 31 kba rare outer membrane protein useful for prepn. of vaccine against syphilis
                                                                                                                                                                                                                                                                                                                                                                                                        Rare outer coat membranes of gradient fractionation, also vaccines, derived antibodies
                                  (SLOK )
                                                                      23-JAN-1997;
                                                                                    31-JUL-1997.
                                                                                                  W09727215-A1
                                                                                                                                                                                                    13-JAN-1998
                                                                                                                                                                                                                   AAT76580
                                                                                                                                                                                                                                AAT76580 standard;
                                                                                                                                                                                                                                                                                                                                  Sequence 957
                                                                                                                                                                                                                                                                                                                                                and other treponemal diseases
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 48-50; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-254907/33.
P-PSDB; AAR79722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blanco. DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                             TROMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                   749 gtaaactccctgctatctt 767
                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                         3 gtgaactccctgctacctt 21
                                                                                                                                                                                                                                                                                               17; Conserv
                                                                                                                                                                                                                                                                                                                                                                          (given in AAR79722) is encoded by DNA isolated using
                                  SIOAN KETTERING INST
UNIV CALIFORNIA.
                                                                                                                                                   pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Champion CI,
                    Lovitt MA,
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                  BP; 210 A; 206 C; 303 G;
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0292904.
94US-0178084.
94US-0255322.
                                                       96US-0599480
                                                                     97WO-US01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US00190
                                                                                                              /*täg= a
/product= immature_TROMP1_protein
                                                                                                                              Location/Qualifiers
1..957
                                                                                                                                                                                                                                DNA; 957 BP
                                                                                                                                                                                                                                                                                                     75.2%;
                    Miller JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lovett
                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                       Spirochaetaceae prodn. - by density isolated immunogenic proteins for u and nucleic acid.
                                         CANCER
                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MA,
                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                            15.8;
                                         RES
                   Tempst PJ;
                                                                                                                                                                                                                                                                                                                                  238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller JN:
                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                             957;
                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                           tryptic
                                                                                                                                                                                                                                                                                                                                                                                                               use in
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                   XFFFXXXX000000000000XX
В
                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                 20-APR-2000
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pathogenic Spirochaetales
                                                                                      detection and induction of immune response in an animal to
                                                                                                                   New isolated Treponema pailidum outer membrane protein -
   Disclosure;
Pages 51-53; 77pp; English
                                                                                                                          used in the
```

This 957 bp sequence (TROMPI gene) encodes a precursor rare outer membrane protein (OMP) of species Treponema pallidum, subspecies pallidum. The TROMPI gene was cloned in a procedure where mixed oligonucleotides (31-A,31-C) hybridized to a EcoRI restriction fragment by Southern blot analysis of T. pallidum genomic DNA. DNA fragments were excised from the agarose gel, purified and ligated into the lambda ZAP II vector and probed with 31-A and 31-C. The phage clones were converted to the pBluescript SK(-) recombinant plasmid by in viomexection. The recombinant expression of these rare OMP's can be used for diagnostic tests to detect syphilis and for development of host immunity during syphilis.

Sequence 957 B₽; 210 A; 206 C; 303 <u>ი</u> 238 T; 0 other;

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Matches
                                           Query Match
Best Local
749
        3 gtgaactccctgctacctt 21
gtaaactccctgctatctt 767
                                   17;
                                           Similarity
                                   Conservative
                                          75.2%;
89.5%;
                                   0,
                                           Pred.
                                           Score 15.8;
Pred. No. 85;
                                   Mismatches
                                                    B
                                                    18;
                                   <u>ب</u>
                                                    Length
                                   Indels
                                                    957;
                                   0;
                                   Gaps
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0

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RESULT 11
AAA67251/c
ID AAA67251 standard; DNA; 537
 31-OCT-2000
                          AAA67251;
(first entry)
                                                 몆
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Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic patransgenic plant; ds. Eucalyptus grandis beta-amylase DNA sequence SEQ ID NO:252

pathway;

Eucalyptus grandis

WO200022092-A2

08-OCT-1999; 99WO-NZ00169

13-OCT-1998; 11-AUG-1999; 980S-0170862. 990S-0148426.

(GENE-) GENESIS RES & DEV CORP LTD.

Bloksberg LN

WPI; 2000-339328/29.

New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant

Claim 1; Page 140; 301pp; English.

The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences,

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AAV04426
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 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 815 sequences of sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or after the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the present invention.
                                                                                                 Calpain is a human leukodyte derived calcium dependent cysteine protease. Calpain can be used to screen for compounds that activate or inhibit its proteolytic activity. Calpain DNA can be used to treat or prevent cancer, cerebral apoplexy, cerebral infarction, subarachnoid haemorrhage, Alzheimer's disease, myodystrophy, cataracts, ischaemic heart disease, atherosclerosis, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calpain; human; leukocyte; calcium dependent cysteine protease; screening; activator; inhibitor; treatment; prevention; cancer; cerebral apoplexy; cerebral infarction; subarachnoid haemorrhage; Alzheimer's disease; myodystrophy; cataracts; collagen disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 537 BP; 155 A; 119 C; 136 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human calpain small subunit cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998
                                                            Sequence 640
                                                                                                                                                                                           The present sequence is a calpain small subunit cDNA fragment.
                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                   Human calpain protein and related DNA - useful for drug screening and treating cancer, stroke, etc.
                                                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP799892-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        small subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV04426 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472 AGTGAAATTCCTGCAACCTT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   schaemic heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                        collagen disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 agtgaactccctgctacctt 21
                                                                                                                                                                                                                       2; Page 38; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                         BP;
                                                                                                                                                                                                                                                                                                                             Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds.
                                                                                                                                                                                                                                                                                                                                                                                       96JP-0083649
                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-0105508
                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA; 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.4%;
85.0%;
72.4%;
                                                         A; 163
                                                                                                                                                                                                                                                                                                                            Shintani Y;
                                                         G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2;
Pred. No. 1.
Score 15.2;
Pred. No. 1.
                                                         223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                         G; 115 T; 0 other;
 DB 18;
L.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
               Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Local Similarity

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps
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AAVOLT 2
AAVOLT 2
AAVOLT 2
AC AAVOLT 27-1
AC AAVOLT 27-
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                                                                                                        Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                           Sequence 804 BP; 181 A; 203 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 35; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP799892-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        small subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calpain; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human calpain small subunit cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV04420 standard; cDNA; 804
                                                                                                                                                                                                                                                                                                                                                                                                       leukocyte derived calcium dependent cysteine protesse. Calpain calbe used to screen for compounds that activate or inhibit its proteolytic activity. Calpain DNA can be used to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening;
                                                                                                                                                                                                                                                                                                                               cancer, cerebral apoplexy, cerebral infarction, subarachnoid
haemorrhage, Alzheimer's disease, myodystrophy, cataracts,
ischaemic heart disease, atherosclerosis, arthritis or coila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes calpain small subunit, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human calpain protein and related DNA - useful for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ischaemic heart disease; atherosclerosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 agtgaactcccaggtgcctt 593
574 agtgaactcccaggtgcctt 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>..</u>
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                          2 agtgaactccctgctacctt 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-482674/45.
                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g; activator; inhibitor; treatment; prevention; cancer; apoplexy; cerebral infarction; subarachnoid haemorrhage; r's disease; myodystrophy; cataracts; collagen disease; r's disease; myodystrophy; cataracts; collagen disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96JP-0083649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0105508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                  72.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shintani Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              បា
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium dependent cysteine protease;
                                                                                                                                  Score 15.2;
Pred. No. 1.
                                                                                                           0;
                                                                                                                                                                                                                                                264
                                                                                                                                                                                                                                                   G; 156 T; 0 other;
                                                                                                                                        .7e+02;
                                                                                                                                                                     DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels 0; Gaps 0;
                                                                                                                                                               Length 804;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calpain can
                                                                                                              0;
                                                                                                              Gaps
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9 7;

Total Lateral

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CC haha43398 to Aba44239. The proteins can have activities based on the CC tissues and cells the genes are expressed in. Example of activities can have activities based on the CC tissues and cells the genes are expressed in. Example of activities can include: cytostatic; proliferative; vulnerary; immunomodulator; cantidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; cc antidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; cc dermatcological; neuroprotective; cardiant; thrombolytic; coagulant; cc polynucleotides and polypeptides can be used for preventing, treating or cc maniforating medical conditions and diagnosing pathological conditions. C polynucleotides, polypeptides, antibodies, agonists and antagonists from ct proventing the proliferation, differentiation or mobilisation of the present invention may be used to treat immune disorders by activating cor inhibiting the proliferation, differentiation or mobilisation of the present invention, graft versus host disease and organ crejection, modulate haemostatic or thrombolytic activity, modulate rejection, cancers, cardiovascular disorders, neurological disease and cc inflammation, cancers, cardiovascular disorders, neurological disease and cc agonists and antagonists may be also be used in drug screens. AAC78449 to catcher the present invention of the present invention of the present invention of the present invention.
                 Query Match
Best Local S
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                                                                                                  Sequence 1242 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 737-738; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
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                                                                                                                                            present invention.
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DB; AAB43556.
17; Conser
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               72.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids comprising sequences encoding peptides
                 Score 15.2;
Pred. No. 1
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                                   Length 1242;
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RESULT 15 AAZ98118/c

AAZ98118 standard; cDNA; 1741

AAZ98118;

11-MAY-2000 (first entry)

Human signal peptide containing protein HSPP-10 cDNA SEQ ä NO:144.

inflammation; cardiovascular disease; anticancer; anti-inflammatory; anti-inflammatory; neuroprotective; cardiovascular; hepatotropic antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzhalmer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy; ss. Human; signal peptide-containing protein; HSPP; diagnosis; hepatotropic; cancer,

Homo sapiens.

WO200000610-A2

06-JAN-2000

26-JUN-1998; 25-JUN-1999; 98US-0090762. 98US-0094983. 98US-0102686. 99WO-US14484

31-JUL-1998; 01-OCT-1998; 98US-0112129

(INCY-) INCYTE PHARM INC

Lal P, Tang Akerblom IE, Bandman O; Au-Young Gorgone . GA, Yue H, Patterson C, Reddy Reddy R, Baughn MR; R, Hillman JL;

WPI; 2000-160673/14. P-PSDB; AAY87233.

New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease

Claim 9; Page 257-258; 327pp; English.

cc be used in gene therapy. HSPP can be used to treat or prevent disorders of activity or function of HSPP. Antagonists of continuing a specific ancient of HSPP. Antagonists of continuing cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, corribosis, poorisis, acquired immune deficiency syndrome, anaemia, corribosis, poorisis, and for the recombinant production of HSPP, for diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP cucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP corribosis and monitoring), in gene therapy, as antisense, correspectic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and correlated diseases (in usual immunoassays), as therapeutic antagonists (potential therapeutic agents). Ab are used to diagnose, or AAZ98109 to AAZ98242 encode AAX87224 to AAX87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anti-cancer, anti-filammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can

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Matches

Conservative

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Mismatches

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Perfect score:
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33.141 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-724-394A-21
US-08-724-394A-22
US-08-724-394A-22
US-08-724-394A-22
US-08-724-394A-21
US-08-726-394-1
US-09-101-826-2
US-09-001-826-2
US-08-366-591B-17
US-08-366-591B-17
US-08-366-591B-17
US-08-368-338-339A-4
US-09-143-214-64
US-09-143-214-64
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US-08-38-38-13661-4
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	- 1 - 50 - 70 - 70		Sequence 1, Appli	Sequence 6, Appli	sequence 20, Appl			Sequence 20. Appl		2	œ.	₩.	Sequence 1, Appli	l. Ap	ω 55	٠.	Sequence 1, Appli	Sequence 3 Appli

## ALIGNMENTS

DNESS: Y: 11 TYPE: SOURC TROMP TROMP TROMP 1:	APPLICATION NUMBER: US/08/5 FILING DATE: 23-JAN-1996 CLASSIFICATION: 435 ATTORREY/AGENT INFORMATION: NAME: Learn, June M. REGISTRATION NUMBER: 31,238 REPERENCE/DOCKET NUMBER: 07 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (619) 678-5070 TELEFAX: (619) 678-5099 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 957 base palls TYPE: nuclelc acid	CORESPONDENCES: 4 CORESPONDENCE ADDRESS: ADDRESSEE: Fish & Richar STREET: 425 Executive S CITY: La Jolla STATE: California COUNTRY: USA COUNTRY: USA LIP: 92037 COMPUTER READABLE FORM: MEDIUM TYDE: Floppy disk COMPUTER: IBM PC COMPATI OPERATING SYSTEM: PC-DOS SOFTWARE: Patentin Relea	US-08-599-480-1  Sequence 1, Application  Patent No. 5753459  GENERAL INFORMATION:  APPLICANT: Blanco, D  APPLICANT: LOVERT,  APPLICANT: LOVERT,  APPLICANT: Champion,  APPLICANT: Tempst,  APPLICANT: Tempst,  TITLE OF INVENTION:  UNIVERSITY.
single near DNA (genomic) E; 1	JAN-1996 3-JAN-1996 435 435 FORMATION: une M. 31,238 MIBER: 31,238 MIDER: 07419/018001 (CIP of INFORMATION: 9) 678-5070 678-5099 ID NO: 1: RISTICS: RESTICS:	ardson P.C. Square, Suite 1400  sk tible OS/MS-DOS ease #1.0, Version #1.	on US/08599480  , David R. , James N. , Michael A. , Michael A. , Cheryl I. , Paul J. ; NUCLECTIDE AND AMINO ACID T. Pallidum RARE OUTER MEM
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US-08-842-199-1
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Patent No. 5821085
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                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/292,904
FILING DATE: 17-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOSTLCh, JUNE M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: PD-3744
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 STRANDEDNESS: 9
TOPOLOGY: linea
MOLECULE TYPE: DN
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Blanco, David R.
APPLICANT: Willer, James N.
APPLICANT: Covett, Michael A.
APPLICANT: Champion, Cheryl I.
APPLICANT: Champion, Cheryl I.
TITLE OF INVENTION: T. PAILIDIM RARE OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEB; Spensley Hern Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 749 GTARACTCCCTGCTATCTT 767
749 GTAAACTCCCTGCTATCTT 767
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Similarity 89.5%;
17; Conservative
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                                                             Conservative
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Pred. No. 19
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RESULT

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RESULT 4
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TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-00190-1
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GENERAL INFORMATION:
APPLICANT: THE RE
                                                                                                                                                                                                                                                       Sequence 16, Application US/08835099A Patent No. 5874277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURENT APPLICATION DATA:
CURENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                                         TITLE OF INVENTION: NOVEL PRITITLE OF INVENTION: AND USE NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, KAZHOTI
APPLICANT: KAWAMOTO, Tombhiro
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bostich, June M.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
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CLONE: TROMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES OF A TITLE OF INVENTION: T. PAILIDUM RARE OUTER MEMBRANE PROTEIN NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      749 GTAAACTCCCTGCTATCTT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..954
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CITY: Los Angeles
                                                                        ADDRESSEE: DIKE, L...
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 06-JAN-1995
                                     COUNTRY:
                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90067
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                                                                  Boston
                     02109
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1880 Century Park East, Suite 500
                                     USA
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                                                                                                       DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.28;
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Pred. No. 19
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US-08-835-099A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16,
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                                                               APPLICATION NUMBER:
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APPLICATION NUMBER: 97105508.2 FILING DATE: 03-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHINTANI, YASUShi
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, TOMOhir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 083649/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 083649/1990
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 AGTGAACTCCCAGGTGCCTT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-6440
                                                  FILING DATE:
                                                                                                 FILING DATE:
CLASSIFICATION:
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STRANDEDNESS: double
                                                                                                                             APPLICATION NUMBER: US/09/157,349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/835,099A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 640 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE;
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                                                               08/835,099
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Pred. No. 36;
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MOLECULE TYPE:

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                                                                                                                                                                                             SOFTWARE: FASCEQ for Windows Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,099
FILING DATE: 04-APR-1997
CLASSIFICATION NOTA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNET/AGENT INFORMATION:
NAME: RESSICK, David S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                            INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 804 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 640 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHINTANI, KA: APPLICANT: KAWAMOTO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL PRINTING OF INVENTION: AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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OPERATING SYSTEM:
                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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linear
cDNA
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Pred. No. 36;
0; Mismatches
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RESULT 8
US-08-724-394A-20/c
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                                                                Matches
                                                                                        Query Match
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Best Local s
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                                                                                                                                                                                                                         NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: SHINTANI, YASU
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomo
574 AGTGAACTCCCAGGTGCCTT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,349
                                                                                                                                                                                                                                                                          NAME: RESNICK, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELECHMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION NUMBER OF SEQUENCES: 18
                  2 agtgaactccctgctacctt 21 ·
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                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: APPLICATION NUMBER: 97105508.2 FILING DATE: 03-APR-1997
                                                                            Local
                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 72.4%; Score 15.2;
Local Similarity 85.0%; Pred. No. 3
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17; Conserv
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                                                           Conservative
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                                                                                                                                                                   linear
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                                                                                                                                                                              double
                                                                    72.4%; Score 15.2;
85.0%; Pred. No. 37;
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                                                        Mismatches
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                                                                                 DB 3;
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                                                                                 Length 804;
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US-08-724-394A-21/c
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                                                                                                                                                            Sequence 21, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: Shin N. APPLICANT: Feder, John N.
                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Meganase --
TITLE OF INVENTION: Sequences and
SECTION: 31
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       1 aagtgaactccctgctacct 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08 FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
                INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                            Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246240 base pairs
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Two Embarcadero Center, 8th Floor
                                                                             Lauer, Peter M.
Ruddy, David A.
                                                                                                             Kronmal,
                                                                                                                              Feder, John N.
                                                                                                                                                                                                                                                                                                                           Conservative
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Tsuchihashi, Zenta
Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
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Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                        72.4%;
                                                                                                           Gregory S.
             Megabase Transcript Map:
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Sequences and Antibodies
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Pred. No. 8
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Query Match
Best Local Similarity
Thes 17; Conserva
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US-08-724-394A-22/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/724
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-576-0300
[NFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
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                                                                                                         ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
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                                                                                                                                                                                                 Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
WOLFF, Roger K.
WENTION: Megabase Transcript Map: No. 587
VENTION: Sequences and Antibodies Thereto
EQUENCES: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Feder, John N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.4%; Score 15.2;
85.0%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                               Gregory S.
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                                                                                                                                                                                                                                      No. 5872237el
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US-08-417-492-1
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Best Local Similarity
Matches 17; Conserv
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                                                            TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
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                                                                                               NAME: Bastlan, Kevin L
REGISTRATION NUMBER: 34,774
REFERENCE,DOCKET.NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                        APPLICATION NUMBER: US/00
FILING DATE: 05-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fitts, Renee A.
REGISTRATION NUMBER: 95,136
REFERENCE/DOCKET NUMBER: 017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115576-0200
                    SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pair
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bennett, Alan B
APPLICANT: Brummell, David A
APPLICANT: Grantz, Alexander
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Grantz, Alexander A
TITLE OF INVENTION: Nucleic Acids Encoding Ascorbate Free
TITLE OF INVENTION: Radical Reductase and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
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LENGTH: 1723 base pairs
TYPE: nucleic acid
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Pred. No. 86;
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APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFREY E.
APPLICANT: HOHOLM, JACK M.
APPLICANT: WIDHOLM, JACK M.
ITILE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
ITILE OF INVENTION: TRANSFORMATION
EILE REFERENCE: UT001.C1
CURRENT APPLICATION NUMBER: US/09/001,826A
CURRENT APPLICATION NUMBER: US/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26
RATLIER APPLICATION WIMBER: US/937,739; 60/025,140
EARLIER APPLICATION WIMBER: US/937,739; 60/025,140
SALTER APPLICATION WIMBER: US/937,739; 60/025,140
EARLIER APPLICATION WIMBER:
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LOCATION:

US-08-417-492-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA (CDNA)
; ORGANISM: Nicotiana tabacum
US-09-001-326-4
                                                                                                                                                                                                                                                                                                 US-09-001-826-25
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GENERAL INFORMATION:
APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFFREY E.
APPLICANT: WIDHOLM, JACK M.
APPLICANT: WIDHOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
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                                                                                                                                                                                                                        Sequence 25, Application US/09001826A Patent No. 5965727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Best Local Similarity
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LOCATION: 49..643
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781..1484
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644..780
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Pred. No. 70
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Pred. No. 68;
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RESULT 14
US-08-366-547-1
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US-08-366-547-1
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LENGTH: 2161
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Best Local Similarity
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CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA (cDNA)
ORGANISM: Nicotiana tabacum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: LOCATION: 90..1940
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2652 base pairs
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Elsenstein, Ronald I.
REGISTRATION NUMBER: 30628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: 4 CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chen, Lan Bo
APPLICANT: Bao, Shideng
TITLE OF INVENTION: A NEW CANCER ASSOCIATED GENE, PROTEIN
TITLE OF INVENTION: EXPRESSED THEREPROM AND USES THEREOF
                                                      FEATURE:
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                                                                                         TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/OFFILING DATE: 30-DEC-1994 CLASSIFICATION: 435
                                    NAME/KEY:
                                                                     TOPOLOGY:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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IBM PC compatible
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Pred. No. 70;
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Search completed: July 25, 2001, 05:18:51 Job time: 9214 sec
                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-276-151-1
                                                                                                                                                    Query Match 70.5%; Score 14.8; Best Local Similarity 88.9%; Pred. No. 74; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              NAME: TOUCHIA, Ph.D., Timothy E
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: ONYX-005/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5481
TELEFAX: (415) 857-0663
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HONDOMY INFORMATION TONA + C MENNA
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US-08-276-151-1/c
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,151
FILING DATE: 14-UU1-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08276151
Patent No. 5597719
GENERAL INFORMATION:
APPLICANT: Freed, Ellen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
NUMBER OF SEQUENCES: 9
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Best Local Similarity
Matches 16; Conserv
                                                                              2436 TEGACTECCTECTACCTT 2419
                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward et al.
STREET: Five Palo ALto Square
CITY: Palo Alto
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130..2076
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88.9%; Pred. No. 72;
ative 0; Mismatches
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REFERENCE
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AQ799987
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Best Local S
                                                                                                                        ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                          106 TIGCTICTGCCAGAGGTT 123
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 53)

1. (Dases 1 to 53)

1. (Manairas; G.G., Mallace, J.G.; Smith, K.; Swartzell; S.; Holzman, T.; Meller, A.; Shaker, R.; Furlong, J.; Young, J.; Zhao, S.; Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                 ttgctcctgccagaggtt 19
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                                                                                                                                                                                            AQ799987 530 bp DNA HATE HS_5300_B2_G10_T7A RPCI-11 Human Male genomic clone Plate-876 Col-20 ROW-N, AQ799987
                                                                                                                    Homo sapiens
                                                                                                                                                          AQ799987.1 GI:5717319
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
Email: Wallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 356)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ068059 356 bp DNA GSS 04-AUG-1998
HS_2200_B2_F03_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2200 Col=6 Row=L, DNA sequence.
AQ068059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Col1 DH10B"
86 c 67 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2200 Col=6 Row=L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CIT Approved Human Genomic Sperm Library D"
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Pred. No. 6.2e+02;
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                                                                                                                              1 (bases 1 to 574)
1 (bases 1 to 574)
1 Tirunagaru, V.G., Sofer, L., Cui, J. and Burnside, J.
An expressed sequence tag database of T-cell-enriched chicken splenocytes: sequence analysis of 5251 clones Genomics 66 (2), 144-151 (2000)
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-345
Fax: 302 831-3651
                                                                                                                                                                                                                                                                                                                                                                            AI979827.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                A1979827 574 bp mrNA EST 10-JUL-2000 pat.pk0004.f2 chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0004.f2 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER-TYPE ALDOLASE), mRNA sequence.
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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17; Conserv
                                                                                                                 Contact: Joan Burnside
                                                                                                                                                                                                                                                           Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                 Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pleter de Jong (pleterédejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 530.
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 Queen Anne Avenue North, Seattle, WA 98109,
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/db_xref-"taxon:9606"
/clone-"Plate-876 Col-20 Row-N"
/clone_lib-"RPCI-11 Human Male BAC Library"
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0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0544 row: H column: 08
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 616)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                         High quality sequence stop: 616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2664475 616 bp DNA
1M0544H08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0544H08 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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                                                                /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical
                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0544H08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                        /note="Vector:
                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                            organism="Mus musculus"
/strain="C57BL/6J"
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/lab_host="E.coli TOP10 F'"
/note="Yector: pcDNA3"
130 c 154 g 125 t
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/db_xref="taxon:9031"
/clone="pat.pk0004.f2"
/clone_lib="chicken activated T cell cDNA"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov Plate: LLCM334 row: n column: 04
High quality sequence start: 2
High quality sequence stop: 608.
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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17; Conservative
                                                         117
            /tissue_type-"choriocarcinoma"
/lab_host="DBHOB (phage-resistant)"
/lab_host="DBHOB (phage-resistant)"
/note="Organ placenta; Vector: POTB7; Site_1: XhoI;
/note="Organ placenta"
/note="Org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:3957315"
/clone_lib-"NIH_MGC_21"
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                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                      Homo sapiens
                                                                                                                                                                                                                                        206 bp mrNA EST 28-OCT-1998
qd72h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735069
                                                                                                                                                                    AI203923.1 GI:3756529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
l (bases 1 to 978)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (phage-resistant,"
/note="Organ: bone; Vector: pcMv-SPORT6; Site_1: Not1;
Site_2: Sal1; cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 250 c 276 g 202 tr
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/clone_lib="NIH_MGC_86"
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/db_xref="taxon:9606"
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Pred. No. 7.
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Pred. No. 6.9e+02;
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1.3e+02;
hes 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 gctcctgccagaggtt 19
                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, N.D., ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares,
                                                                                                                               Unpublished (1997)
                                                                                                                                                Tumor Gene Index
                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                aa60a05.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825296 3',
                                                                                                                                                                                                                                                       Homo sapiens
CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                            mRNA sequence
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Seq primer: -40UP from Gibco
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Insert Length: 1344 Std Error: 0.00
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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1 (bases 1 to 206)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1735069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_testis_NHT"
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Pred. No. 9.1e+02;
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                                                              Ph.D., David Allman,
                                 Ph.D.,
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                                    M. Fatima
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                                                         www-bio.llni.gov/bbrp/image/image.html
Insert Length: 919 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 181.
                                                                                                                            CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                 Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA5/7/198 341 bp mRNA EST 12-SEP-1997 nm87/bl1.sl NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1075197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                      Inpublished (1997)
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www-bio.llni.gov/bbry/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 320.
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Similarity 100.08;
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                                        Location/Qualifiers
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constructed by Bento Soares and M. Fatima Bonaldo ^{\rm 4} 71 c \, 68 g \, 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="germinal center B cell"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_GCB1"
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Pred. No. 9.9e+02;
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VERSION
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AQ751483
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JOURNAL COMMENT

REFERENCE

AUTHORS TITLE

ACCESSION VERSION

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SOURCE

ORGANISM

KEYWORDS

RESULT 1 AA577198

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FEATURES

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189 GCTCCTGCCAGAGGTT 204
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                                                                                                                                                                                                                                                                                  Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                         Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (Pieterdel-jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 1152 row: D column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU/51483 738 bp DNA GSS 19-JUL-1999
HS_5576_B2_B02_SP6 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1152 Col=4 Row=D, DNA sequence.
AQ751483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shakar,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases i to 738)
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                                                                                                                                                                                                                             quality sequence stop: 738.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jwallace@u.washington.edu
                                                                              /db_xref="taxon:9606"
/clone="Plate=1152 Col-4 Row-D"
/clone_11b="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen d
                                                                   /sex-"male"
                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Bento Soares and M. Fatima Bonaldo (Soares4
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/clone_lib="NCI_CGAP_Co9"
/tlssue_type="colon tumor RER+"
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o. 9.9e+02;
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Best Local Similarity 89.59
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JOURNAL
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1 (bases 1 to 15)

1 (bases 1 to 15)

1 (lark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tun,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 627___Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W25430 115 bp mRNA EST 10-0CT-1996 zb90c01r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:310848 5', mRNA sequence.
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                                                                                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                                                                                                                                        /db_xref="taxon;9606"
/clone="IMAGE;310848"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:1254262"
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1. .115
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a 167 c 190 g 203 t
                             83.2%;
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100.0%; Pr
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Pred. No. 1.1e+03; Indels 0;
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0; Mismatches
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2; Indels - 0; Gaps >0;
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Search completed: July 25, 2001, 04:54:56 Job time: 10429 sec

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                                                                                                                                                                                                                                                                                   Score
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/SIDS1/9cgdata/geneseg/genesegn/Na1981.DAT:*
/SIDS1/9cgdata/geneseg/genesegn/Na1982.DAT:*
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UGT1*1 gene exon 1
Upstream DNA seque
3'-flanking region
Collagen IV alpha
Human Alport syndr
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	AAF54721	2	2724	4.0			
	AAF54722	-	2171	4.0	8		
	AAN60895		2059	4.0	œ		
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	AAQ24919	3	1226	4.0			
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## ALIGNMENTS

RESULT AAT79543

AAT79543 standard; DNA;

20 ВP

UGT1\*1 gene exon 1 upstream PCR primer C.

23-JAN-1998 AAT79543;

(first entry)

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Improving drug trial efficiency comprises identifying participants
                            WPI; 1997-448702/41.
                                                                                                16-MAR-1996;
01-MAR-1996;
                                                                                                                                03-MAR-1997;
                                                                                                                                                       04-SEP-1997
                                                                                                                                                                                                                           Uridine diphosphate glucuronosyltransferase gene; UGT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigier-Najjar; type 2; drug metabolism; Drug trial efficiency; screening; PCR primer; ss.
                                                                          AIND (-DOLD)
                                                                                                                                                                             WO9732042-A2
                                                                                                                                                                                                               Synthetic.
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Is a mild, common form of unconjugated hyperbilirubinaemia associated with reduced bilirubin glucuronidation capacity. Analysis of the genetic CC basis of GS has allowed 2 forms to be identified. One is a mild form CC associated with a homozygous 2 bp insertion in the TATA sequence CC upstream of the UCT1*1 exon 1, and the other is a more severe form CC associated with heterozygosity for a mutation which, when homozygous, CC causes Crigler Najar type 2 disease. The first form is autosomal cC recessive and the second is inherited dominatly. Patients suffering from CC GS, which is benign, may have altered metabolism of some drugs, making it CC difficult to determine if an effect is due to the drug or the syndrome. CC Drug trial efficiency would be improved if potential participants can be CC sceened for the genetic basis of GS, and eliminated or included on CC basis of them possessing or not possessing GS.
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                                                                                                                                                                                                                                                                                                                                                                                          GC_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uridine diphosphate glucuronosyltransferase gene; UCT; Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler-Najjar; type 2; drug m
                                                                                misc_feature
                                                                                                                                                       protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Upstream DNA sequence of UGT1*1 gene exon 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 7 A; 6 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upstream of the uridine diphosphate glucuronosyltransferase (UGT) 1*1 exon 1 (see AAT79540), and was used to amplify fragments of 9 bp. This gene is known to be associated with Gilbert's syndrome (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This PCR primer
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ilarity 100.0%;
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317..324
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180. 191
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Pred. No. 0.11;
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Score 20; DB 1 Pred. No. 0.19; Mismatches

DB 18; 0;

Length 620; Indels

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Sequence 620 BP; 157 A; 127 C; 151 G; 185 T; 0 other;

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Insertion in the TATA sequence upstream of the UGTI*1 exon 1, and the other is a more severe form associated with heterozygosity for a mutation which, when homozygous, causes Crigler-Najjar type 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on basis of them possessing or in this case, screening involves PCR amplification of the UGT gene, using the primers described in AAT79541-44.
                                                                                                                                                                                                                                                                                                                                       This sequence represents the upstream sequence, positions -611 to 9 in the patent, of uridine diphosphate glucuronosyltransferase (UCT) gene 1*1 exon 1. This gene is known to be associated with Gilbert's syndrome (GS). GS is a mild, common form of unconjugated hyperbilirubinaemia associated with reduced bilirubin glucuronidation capacity. Analysis of the genetic basis of GS has allowed 2 forms to be independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 2 by independent of the syndrome is a mild form associated with a homozygous 3 by independent of the syndrome is a mild form associated with a homozygous 3 by independent of the syndrome is a mild form associated with a homozygous 3 by independent of the syndrome is a mild form associated with a homozygous 3 by independent of the syndrome is a mild form associated with a homozygous 3 by independent of the syndrom
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01-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a PCR primer used in the present CC invention. The present invention describes an in vitro method of diagnosis of a disease in an animal. The method comprises determining CC the genotype of an interleukin-6 (IL-6) gene in the animal. The invention also describes: (1) a method of identifying an animal predisposed or susceptible to a disease, comprising determining the genotype of an IL-6 gene in the animal; (2) a composition for use in C diagnosing a disease in an animal, the composition comprising one or more primer nucleic acid molecules adapted to amplify a portion of a 3' flanking region of an IL-6 gene in the animal predisposed or susceptible to a disease, the composition comprising one or more primer nucleic acid molecules adapted to amplify a portion of a 3' flanking region of an IL-6 gene in the animal. The method can be used for the diagnosis of carticularly of predisposition or susceptibility to a disease,
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
                                             AAZ57627 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determination of genotype of an II-6 gene in an individual for diagnosis of or identification of a predisposition or susceptibility to a disease, particularly osteoporosis
                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 4 A; 4 C; 7 G; 7 T; 0 other;
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nilarity 94.4%;
Conservative
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  Human Alport syndrome oligonucleotide #1.
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to disease)
(b) predict
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23-DEC-1998;
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target general associated with particular diseases. The mutant variant represented by this sequence gives rise to Alport syndrome phenotype. The specification lists approximately 2500 genes that are target groups for the nucleotide probes of the invention. The probes are used to determine the genomic profile of an individual, particularly for:

(a) prognosis and management of disease (or determining susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  likelihood of developing disease.

Antibodies specific for the proteins encoded by the genes in the target list, can be used similarly. Identification of a core group of genes associated with disease, makes possible the use of genetic profiling as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is an collagen IV alpha 3 deletion mutant fragment. The mutated gene is an example of a variant that can be detected using the nucleotide probes of the invention. The probes consist of complementary DNA or RNA for the detection of variants in a group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide probes used in genetic screens for determining genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alport syndrome; disease prognosis; health screening; health management tool; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen IV alpha 3; deletion mutant; nucleotide probe; genomic profile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen IV alpha 3 deletion mutant fragment #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          universal health management tool.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (b) predicting a patient's response to therapy and symptom profiles; (c) for health screening; (d) for health screening; (d) to develop new strategies for therapy and clinical trials; and (e) to construct health management algorithms or models, e.g. of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 25; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              profiles, e.g. for prognosis or management
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOSTIC PHARMA LTD
                                                                                                                                                     8 toaccegacacagtcaaac 26
                                                                                                                                                                                           2 tcacgtgacacagtcaaac 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0012098.
98GB-0028289.
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                                                                                                                                                                                                                                                                                                                        Score 15.8;
Pred. No. 19;
                                                                                                                                                                                                                                                                                               Mismatches
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Indels

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Pred. No. Mismatches

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of are mutations or polymorphisms. Included in the specification are lists are mutations or polymorphisms. Included in the specification are lists of genes for the following target groups: (1) ADME (absorption, citibution, metabolism and elimination - about 1000 genes); (2) ADME (absorption, citi) oncology (about 1200 genes); (1) ADME (absorption, citi) oncology (about 1200 genes); (1) central nervous system (about 1200 genes); (1) personality (about 500 genes); (2) personality (about 500 genes); (2) personality (about 1200 genes); (2) personality (about 500 genes); (2) immunology (about 1100 genes); (2) personality (about 1200 genes); (2) personality (about 1100 genes); (2) personality (about 1100 genes); (2) personality (about 1100 genes); (2) personality (about 12) genes); (2) personality (2) per
Sequence 27 BP; 7 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes new nucleotide probes (I) comprising complementary DNA or RNA, used in the detection of variants in a ground formula of the comprising comprising comprising compressions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 25; 745pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide probes used in genetic screens for determining genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-097547/08
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05-AUG-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-1998
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e.g. for prognosis or management -

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Human; glycogen storage disease 2; genetic filing; identification; polymorphic variation; mutation; detection; probe; prognosis; headache; gene associated disease; health screening; therapy; clinical trial; absorption; distribution; metabolism; elimination; oncology; dementia; central nervous system; behaviour; brain injury; psychosis; personality; cardiovascular; gastrointestinal; respiratory; immunology; development;
                                                                      98GB-0016086
98GB-0016921
98GB-0017097
98GB-0017200
98GB-0017632
                                                                                                                                                             98GB-0016085.
                                                                                                                                                                                                                                  98GB-0014580
                                                                                                                                                                                                                                                                                                                     98GB-0012099
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                                                                                                                   Cancer; human; colon; breast; lung; transmembrane receptor; ATPase; integral membrane protein; aspartyl protease; GATA family; wnt family; phorsoription factor; G-protein alpha subunit; protein phosphatase; phorbolester binding protein; diacylglycerol binding protein; trypsin; protein kinase; tyrosine phosphatase; developmental signalling protein; description; diagnostic; genetic mapping; diagnostic; detection; treatment; cervical; melanoma; colorectal adenocarcinoma; wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma; lung carcinoma;
         08-JUL-1999
                                           W09933982-A2
                                                                           Homo sapiens
                                                                                                              prostate;
                                                                                                                                                                                                                                                                                          Human cancer cell derived cDNA #241.
                                                                                                          eukemia; lymphoma; dysplasia; hyperplasia; endometrium;
                                                                                                                                                                                                                                                                                                                                     24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                               AAX98515 standard; cDNA; 300 BP
                                                                                                                                                                                                                                                                                                                                                                         AAX98515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 tcacccgacacagtcaaac 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tcacgtgacacagtcaaac
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07-JUL-1998; 16-JUL-1998;

27-JUN-1998;

24-JUN-1998

-JUN-

04-JUN-1999;

16-DEC-1999

W09964627-A2 Homo sapiens

18-JUL-1998;

24-JUL-1998

21-OCT-1998; 27-OCT-1998; Stache-Crain B, Jones LW, Kassam A, Lamson G, Leshkowit; 03-APR-1998; 21-OCT-1998; (CHIR ) Crkvenjakov R, Escobedo J, 21-DEC-1998; 22-DEC-1998; CHIRON CORP. HYSEQ INC. Leshkowitz D, Garcia PD, Dickson M, Drmanac K, Liming MA; Jarcia PD, Garcia V, Giese K, Innis MA; Jaam A, Kennedy GC, Kita D, Labat I; Shkowitz D, Pot D, Randazzo F, Reinhard 98US-0080664. 98US-0105234. 98US-0105877. 98US-0217471 98WO-US27610.

WPI; 1999-430243/36

New isolated human polynucleotides

Claim 1; Page 375; 591pp; English.

CC by screening for differential expression in colon cancer. Dreast cancer CC and lung cancer cell lines. The polynuclectides of the invention are CC represented in AAX98275-X99118 and encode polypeptides of protein CC families selected from 4 transmembrane segments integral membrane compromers. Transmembrane receptors, ATPases associated with various CC cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, CC signalling proteins and WM/Tsp5/WWP domain containing proteins. The CC encoded polypeptides also have a functional domain selected from Ank CC concodomain, Est-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CCHC class), and zinc-binding metalloprotease This invention describes novel isolated human polynucleotides obtained

Query Match

79.0%; Score 15.8; DB 21; Length 27;

3 G; 7 T; 0 other;

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RESULT AAASO369
ID AAAS
XX AAAS
XX AAAS
XX AAAS
XX AAAS
XX COAN
AC COA
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                                                                                                                                          Claim 25; Page 153-154; 158pp; English,
                                                                                                                                                                                                                      Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saus J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY95920.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-572094/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAUS/) SAUS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GTCAGGTGACAGAGTCAAA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9905-0121483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= Met-deleted GPDeltaIII/IV/V
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..210
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Pred. No. 2
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The present sequence is that of cDNA encoding human Goodpasture antigen (GP) DeltaIII/IV/V (see AAY95920), an alternative form of human GP resulting from splicing out of exons III, IV and V. The

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The present sequence is that of cDNA encoding human Goodpasture antigen (GP) DeltaIII/V (see AAY95921), an alternative form of human GP resulting from splicing out of exons III and V. The CDNA was obtained by subcloning a cDNA encoding the protein into a modified perish vector including an initiator Met. The invention relates to novel Goodpasture antigen binding proteins (GPBPs, see AAY95900-11), which bind to and phosphorylate the unique N-terminal region of human GP, and which are highly expressed in several

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA was obtained by subcloning a cDNA encoding the protein into a modified pETISb vector including an initiator Met. The invention relates to novel Goodpasture antigen binding proteins (GPBPs, see AAY9500-11), which bind to and phosphorylate the unique N-terminal region of human GP, and which are highly expressed in several autoimmune conditions. Claimed methods for treating an autoimmune disorder, cell apoptosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived poptide, such as GPDeltaIII/IV/V or a nucleic acid sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                  Claim 25; Page 154-155; 158pp; English.
                                                                                                                                           Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodpasture antigen; GPDeltaIII/V; human; GPBP; goodpasture antigen binding protein; autoimmune disease; apoptosis;
                                                                                                                                                                                   P-PSDB; AAY95921
                                                                                                                                                                                                  WPI; 2000-572094/53.
                                                                                                                                                                                                                           Saus J;
                                                                                                                                                                                                                                                                                24-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; tumour;
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                                                                                                                                                                                                                                                     (SAUS/) SAUS J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                99US-0121483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..219
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/product= Met-deleted GPDeltaIII/V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%;
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Pred. No. 29;
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AAA50368
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                                  The present sequence is that of cDNA encoding human Goodpasture antigen (GP) DeltaIII (see AAYSS919), i.e. an alternative form of human GP resulting from splicing out of exon III. The cDNA was obtained by subcloning a cDNA encoding the protein into a modified to novel Goodpasture antigen binding proteins (GPBPS, see 1940n of human GP, and which are highly expressed in several autoimmune conditions. Claimed methods for treating an autoimmune and to not protein for the second conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                            Claim 25; Page 152-153; 158pp; English.
            disorder, cell apoptosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived
                                                                                                                                                                                                Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis
                                                                                                                                                                                                                                                      P-PSDB; AAY95919
                                                                                                                                                                                                                                                                 WPI; 2000-572094/53.
                                                                                                                                                                                                                                                                                                 Saus J;
                                                                                                                                                                                                                                                                                                                                                                      24-FEB-2000; 2000WO-IB00324
                                                                                                                                                                                                                                                                                                                         (SAUS/)
                                                                                                                                                                                                                                                                                                                                                  24-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                W0200050607-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodpasture antigen; GPDeltaIII; human; GPBP; goodpasture antigen binding protein; autoimmune disease; apoptosis; cancer; tumour; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Goodpasture antigen DeltaIII cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA50368 standard; DNA; 680 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA50368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune conditions. Claimed methods for treating an autoimmune disorder, cell apoptosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived peptide, such as GPDeltaIII/V or a nucleic acid sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 507 BP; 159 A; 113 C; 104 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 tcacccgacacagtcaaac 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 tcacgtgacacagtcaaac 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                       SAUS
     such as GPDeltaIII or a
                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                              9908-0121483
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=_ a
/product=_Met-deleted_GPDeltaIII
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB
sequence encoding it.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Sequence 680 BP; 204 A; 159 C; 145 G; 172 T; 0 other;
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RESULT 10
AAA50367
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                            Human Goodpasture antigen DeltaV cDNA
                                                                                                                                                                                                           gene therapy; ss.
                                                                                                                                                                                                             GOOdpasture antigen; GPDeltaV; goodpasture antigen binding protein; GPBP; human; autoimmune disease; apoptosis; cancer; tumour;
                                                                                                                                                                                                                                                  AAA50367;
                                                                                                                                                                                                                                                          AAA50367 standard; DNA; 685
                                                                                                                                                                                                                                         20-NOV-2000
                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                       2 tcacgtgacacagtcaaac
                                                                                                                                                                                                                                                                                   tcacccgacacagtcaaac
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                           79.0%;
                                                                                                                                                                                                                                                                                   83
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Pred. No. 32;
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                   0
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CDS /product= /partial Location/Qualifiers
1..636 /\*tag-Met-deleted GPDeltay

Homo sapiens

Saus J; 24-FEB-1999; 24-FEB-2000; 2000WO-IB00324 (SAUS/) SAUS 31-AUG-2000. WO200050607-A2 9908-0121483

WPI; 2000-572094/53. P-PSDB; AAY95918

The present sequence is that of cDNA encoding human Goodpasture antigen (GP) DeltaV (see AAY95918), i.e. an alternative form of human GP resulting from splicing out of exon V. The cDNA was obtained by subcloning a cDNA encoding the protein into a modified to novel Goodpasture antigen binding proteins (GPBPs, see AAY95900-11), which bind to and phosphorylate the unique N-terminal autoimmune conditions. Claimed methods for treating an autoimmune disorder, cell apoptosis or a tumour involve modifying the expression or activity of GPBP, especially using a GP-derived neartife annex a condition. Claim 25; Page 150-151; 158pp; English. Novel Goodpasture antigen binding proteins useful for diagnosing and treating autoimmune disorders, tumor, and preventing cell apoptosis

Sequence 685 BP; 206 A; 157 C; 138 G; 184 T; 0 other;

peptide, such as GPDeltaV or a nucleic acid

sequence encoding it.

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Query Match
            Local Similarity
   Conservative
          79.0%;
    0;
          Score 15.8;
Pred. No. 32;
  Mismatches
                DB 21;
  2
                 Length 685;
0;
Gaps
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RESULT 11

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65 tcacccgacacagtcaaac

8 20

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68 tcacccgacacagtcaaac

86

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Oy 2 tenegtgacacagtcanac 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the human type IV collagen alpha 3 chain. CC The present invention describes an isolated protein chosen from the NCI C domain of the alpha 1 alpha 2 or alpha 3 chains of type IV collagen or a fragment, analogue, derivative or mutant, which has anti-angiogenic properties. The anti-angiogenic proteins, multimers and chimeras are useful for inhibiting angiogenic activity in mammalian tissue, especially for treating diseases chosen from angiogenesis-dependent cancers, benign tumours, rheumatoid arthritis, diabetic retinopathy, psoriasis, coular angiogenesis diseases, osler-webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, adhesions, atherosclerosis, scheroderma, hypertrophic scars, cat scratch adhesions, atherosclerosis, scheroderma, hypertrophic scars, cat scratch stenosis, contraception and obesity. The compositions can be used to inhibit a disease characterised by analogenic activity, in conjunction
                                                     Matches
                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-angiogenic proteins comprising the NCI domain of the alpha 1, 2 or 3 chain of Type 1V collagen used in, e.g. treatment of benigh tumors and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9965940-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; type IV collagen; anti-angiogenic; angiogenesis; cancer; benign tumour; rheumatoid arthritts; diabetic retinopathy; psoriasis ocular angiogenesis disease; Osler-Webber Syndrome; telangicetasia; myocardial angiogenesis; plaque neovascularisation; angiofibroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ57158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ57158 standard; cDNA; 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 33; Fig 16A; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1998;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-2000
                                                                                                                                       Sequence 738 BP; 204 A; 184 C; 162 G; 188 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BETH-) BETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contraception;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis; scleroderma; hypertrophic scar; cat scratch disease,
                                                                                                                                                                          with radiation therapy, chemotherapy or immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human type IV collagen alpha 3 chain nucleotide sequence SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-097708/08
                                                                     Similarity
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0089689.
99US-0126175.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obesity; ss.
                                                                     79.08;
                                                   Score 15.8; In Pred. No. 32; 0; Mismatches
                                                                                      BB
                                                                                       21;
                                                     <u>ب</u>
         Length 738;
                                                      Indels
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                                                     Gaps
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Disclosure; Fig 17c; 56pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ache rosacea; phylectenulosis; syphilis; Mycobacteria infection; lipid degeneration; chemical burn; ulcer; herpes simplex infection; Herpes zoster infection; protozoan infection; Kaposi's sarcoma; Mooren ulcer; Terrien's marginal degeneration; marginal keratolysis; trauma; systemic lupus; polyarteritis; megener's sarcoldosis; scleritis; Steven's Johnson disease; radial keratotomy; sickle cell anaemia; sarcold; pseudoxanthoma elasticum; Pager's disease; vein occlusion; artery occlusion; carotid obstructive disease; chronic uveitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic vitritis; Lyme's disease; Eales disease; Bechets disease; myopia; optic pit; Stargart's disease; pars planitis; chronic retinal detachment; hyperviscosity syndrome; twoplasmosipost-laser complication; fibrovascular tissue proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vitamin A deficiency; contact lens overwear; atopic keratitis; superior limbic keratitis; pterygium keratitis sicca; sogrens;
Inhibition of angiogenesis with non-collagenous alpha chain monomer useful for treating e.g. tumor growth or metastasis, neovascularisation, etc.
                                                                                                                               Hudson BG,
                                                                                                                                                                                                                                                                                              07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ulceritive colitis; psoriasis; atherosclerosis; pemphigoid; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corneal graft rejection; neovascular glaucuma; retrolental fibroplasia; epidemic keratoconjunctivitia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corneal neovascularization; retinopathy of prematurity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       choroidal neovascularization; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type IV collagen; NCl domain; non-collagenous domain; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type IV collagen NC1 domain alpha-3 monomer DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ20091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA220091 standard; DNA; 900
                                                                        WPI; 1999-601297/51.
P-PSDB; AAY31993.
                                                                                                                                                                  (UNIV ) UNIV KANSAS MEDICAL CENT
                                                                                                                                                                                                      27-MAR-1998;
29-OCT-1998;
                                                                                                                                                                                                                                                            26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                  WO9949885-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemangiona; Osler-Weber-Rendu; AIDS; ocular neovascular discase; osteoarthritis; chronic inflammation; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                               Sarras MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour;
                                                                                                                                                                                                    98US-0079783
98US-0106170
                                                                                                                                                                                                                                                          99WO-US06445
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
40..90
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                       /product= "BM40 signal peptide"
91..843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 40..846
                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/product= "affinity-tagged alpha-3 monomer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retinal neovascularization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis; therapy; diabetic retinopathy;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mooren ulcer, Terrien's marginal degeneration, marginal keratolysis, trauma, systemic lupus, polyarteritis, Wegener's sarcoidosis, scleritis, Steven's Johnson disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma elasticum, Pagets disease, vein occlusion, artery occlusion, carctid obstructive disease, Echeroic uveitis, chronic vitritis, Lyme's disease, Eales disease, Bechets disease, myopla, optic pits, Stargarts disease, pars planitis, chronic retinal detachment, hyperviscosity syndromes, toxoplasmosis, post-laser complications, abnormal proliferation of fibrovascular tissue, haemanguomas, Oster-Weber-Rendu, AIDS, ocular neovascular disease, osteoarthritis, chronic inflammation, Crohn's disease, ulceritive colitis, psoriasis, atherosclerosis, and pemphigoid (all
                                                          tumour growth; integrin receptor; carcinoma; sarcoma; rhabdomyosarcoma; retinoblastoma; Ewing sarcoma; neuroblastoma; osteosarcoma; leukaemia; diabetic retinopathy; rheumatoid arthritis; neovascularisation; muscular degeneration; corneal graft rejection; vitamin A deficiency; atopic keratitis; Mycobacteria infection; chemical burn; sarcoid; Kaposi's sarcoma; sickle cell anaemia; carcitd obstructive disease; chronic inflammation; psoriasis; therapy; alpha3(IV)NC1; ds.
                                                                                                                                                                                                                              Type IV collagen alpha chain monomer; human; inhibitor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroplasia, epidemic keratoconjunctivitis, vitamin A deficiency, contact lens overwear, atopic keratitis, superior limbic keratitis, pterygium keratitis sicca, sogrens, acne rosacce, phylectenulosis, syphilis, mycobacteria infections, lipid degeneration, chemical burns, bacterial ulcers, fungal ulcers, herpes simplex infections, herpes zoster infections, protozoan infections, Kaposi's sarcoma, herpes zoster infections, protozoan infections, Kaposi's sarcoma,
                       Homo sapiens
                                                                                                                                                                                                                                                                                 Human alpha3(IV)NC1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA90993 standard; DNA; 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monomers can be produced via recombinant protein expression. The polynucleotides and polypeptides are used to treat an angiogenesis-mediated disorder or condition, especially selected from solid and blood-borne tumours, diabetic retinopathy, remarked arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the extracellular matrix, each method comprising contacting the tumour or animal tissue with 1 or more isolated type IV collagen NCI alpha chain monomer(s) selected from the group consisting of alpha-1, alpha-2, alpha-3 and alpha-6 NCI chain monomers. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mature protein comprising an affinity tag (facilitates purification and identification of the material) and the alpha-1 chain monomer. The invention provides methods and kits for inhibiting angiogenesis, the invention growth and metastasis, and endothelial cell interaction with
                                                                                                                                                                                                                                                                                                                                       12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinal neovascularization, choroidal neovascularization, macular degeneration, corneal neovascularization, retinopathy of prematurity, corneal graft rejection, neovascular glaucoma, retrolental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence of a recombinant DNA encountrype IV collagen non-collagenous (NCI) domain alpha-3 polype (see AAV31993) composed of a BM40 signal sequence (which is from the mature protein) to facilitate protein secretion, and the mature protein) to facilitate the contribution of the mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tcacgtgacacagtcaaac 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcacccgacacagtcaaac 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide sequence of a recombinant DNA encoding
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 228 A; 243 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-collagenous (NCI) domain alpha-3 polypeptide omposed of a BMAN signal accuracy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.8;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 G;
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REFERRATION OF THE STAND OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     designated alpha3(IV)NC1. The invention relates to a medicine inhibiting angiogenesis, tumour growth or metastases, or endothelial cell interactions with the extracellular matrix, comprising contacting the cells or tissue with a polypeptide composition containing antagonists of specific integrin receptors. The methods and the antagonists are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a human type IV collagen alpha chain monomer, designated alpha 3(IV)NCI. The invention relates to a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 17c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of antagonists of specific integrin receptors for inhibiting angiogenesis, tumour growth or metastases, or endothelial cell interactions with the extracellular matrix
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DB; AAY97555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78pp; English
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carcinomas, sarcomas, rhabdomyossrcoma, retinoblastoma, Ewing sarcoma, neuroblastoma, osteosarcoma or leukaemia). These are also applicable to treating non-tumourigenic diseases and conditions with accompanying undesired angiogenesis, e.g. diabetic retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal neovascularisation, muscular degeneration, corneal graft rejection, vitamin A deficiency, atopic complications, chronic inflammation or psoriasis. keratitis, Mycobacteria infections, chemical burns, Kaposi sickle cell anaemia, sarcoid, carotid obstructive disease, useful for treating diseases and conditions with accompanying undesired anglogenesis, e.g. solid and bicof-borne tumours (e.g. melanomas, for inhibiting angiogenesis, tumour growth or metastases, or endothelial cell interaction with the extracellular matrix. The antagonists are also Kaposi's sarcoma post-laser

₽P; 228 A; 243 C;

206

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223 T;

0 other;

Sequence 900

Ş Matches Query Match Local 2 tcacgtgacacagtcaaac 20 Similarity Conservative 79.0%; 0; Pred. No. Score 15.8; Mismatches BB 'n Length 900; Indels 0, Gaps

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AAF13921, ID AAF1 g AAF13921 standard; cDNA; 1276 176 tcacccgacacagtcaaac 194

13-MAR-2001 AAF13921;

(first entry)

Aspergillus oryzae EST SEQ ID NO:6444.

Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc same genes in one or more second filamentous fungal cells. Monitoring ct the global expression of genes from FF cells allows the production of discovered, possible functions of unknown open reading frames can be considered. The expression of genes can be used to study how FF cells and genes in culture conditions, environmental stress, spore compingenesis, recombination, metabolic or catabolic pathway can be engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an CC engineering. Using ESTs provides several advantages over genomic or catabolic pathway equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate canalysis of the results. AAF01478 to AAF11253 represents ESTs from Aspergillus oryzae; and CC niger; AAF11854 to AAF11858 represents ESTs from Aspergillus oryzae; and CC AAF14879 to AAF11853 represents ESTs from Trichoderma reesei, which are call general advantaged on the constitution of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
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                          Hybridiaation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all specifically claimed in the present invention.
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                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 12176.
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99US-0140823. 99US-0140991. 99US-0141287. 99US-0141842. 99US-0142154.

02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 109-JUL-1999; 11-JUL-1999; 14-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

> 99US-0142390, 99US-014280, 99US-014280, 99US-0142920, 99US-0142977, 99US-0143542, 99US-0143624, 99US-0144005,

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(c) 1993 - 2000 compugen Ltd.
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US-08-05-3-131-45

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270, App
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             1, Appli
239, App
189, App
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47, Appl
215, App
215, Appl
49, Appli
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US-08-857-464-3/c
US-08-857-464-3/c
; Sequence 3, Application US/08857464
; Patent No. 6066450
; Patent No. 6066450
; GENERAL INFORMATION: Stuart H.
; APPLICANT: Grant, Struan F.A.
; APPLICANT: Grant, Struan F.A.
; TITLE OF INVENTION: Diagnostic an
                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-857-464-3
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 961028
FILING DATE: 16-MAY-1996
FITORNEY/AGENT INFORMATION:
NAME: ESMOND, RODERT W.
REGISTRATION NUMBER: 32-893
REGISTRATION NUMBER: 1581
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2640
                                                                                                                                                                                                                                                    TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,464
APPLICATION NUMBER: US/08/857,464
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ADDRESSEE: STERNE, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-MAY
CLASSIFICATION: 435
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US-08-757-669A-18
US-08-480-784-40
US-08-483-553-40
US-08-483-554-8-40
US-08-488-0118-40
US-08-850-727-40
US-08-850-727-40
PCT-US95-10203-40
PCT-US95-10203-4
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                                                         ; Score 16.4; DB; Pred. No. 4.2; 0; Mismatches
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Query Match

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GENERAL INFORMATION:
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Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
APPLICANT: FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-49
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                 ITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED ITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                    74 TCACGTGACTCAGCCAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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APPLICATION NUMBER: US/08/991,789A

FILING DATE: 11-Dec-1997

CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Frudakis, Tony N.
                 Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 519 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 210121.419C3
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Massachusetts
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STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%;
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Pred. No. 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                    TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 154:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
     SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pair
                                                                       NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
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NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROMMENS, JOHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED ITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                   APPLICATION NUMBER: US/08/592,541 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02110
                                                                                                                                                 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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High Street Tower - 125 High Street
1990 base pairs
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Pred. No. 4
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-592-541-154
RESULT 6 0-154 US-09-127-480-154, Application US/09127480 H. CALLER OF SECTION US/09127480
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US-09-124-698-154
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Best Local
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ST. GEORGE-HYSLOP,
APPLICANT: ROMNENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SE
TITLE OF INVENTION: TO ALZHEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                 168 TCAAGTGACCCAGNCAAAC 186
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                                                                                                                                                                                 Local Similarity 84.3 ies 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                      74.0%; Score 14.8;
84.2%; Pred. No. 49
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                      DB 4; Length 1990;
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US-08-496-841C-154
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                                                                                                                                                                                                                                                                                                                                                            Sequence 154, Application US/08496841C Patent No. 6210919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 154:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                IP: 10022
COMPUTER REALABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                 APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02110
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                                                                                                                    COUNTRY:
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                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%; Score 14.8;
84.2%; Pred. No. 49;
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US-08-100-247-4
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Matches 16; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                           NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: OBRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                           NFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 154: SEQUENCE CHARACTERISTICS:
                      MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C
COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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APPLICANT: KISHIMOTO, YASUO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 TCAAGTGACCCAGNCAAAC 186
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US
FILING DATE: 19930730
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92660
                                                                                                                                                                                                   TELEFAX: 619-235-0176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 154:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: CUAKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Febhiner, Ph.D.
REGISTRATION NUMBER: 35,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1990 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: KNOBBE, MARTENS, OLSON AND BEAR 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                      US-08-232-513A-5
Sequence 5, Application US/08232513A
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; CLONE: PROSAPOSIN CDNA US-08-100-247-4
                                                                                                                                     ; MOLECULE TYPE: CDNA
US-08-483-146A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08483146A Patent No. 5696080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserv
                                                          Matches
                                                          Best Local Similarity
Matches 16; Conserv
                                                                                         Query Match
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                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1194 TCACGTGACTCAGCCAAA 1211
1194 TCACGTGACTCAGCCAAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
ODERATING SYSTEM: DOS
SOFTWARE: FastsEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,146A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                   NAME: ISTACISC, Ned A RECISTATION NUMBER: 29,655 RECERRICE/DOCKET NUMBER: MYI TELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: O'Brien, John S. APPLICANT: Kishimoto, Yasuc
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                STRANDEDNESS:
              2 tcacgtgacacagtcaaa 19
                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.A
                                                                                                                                                                                                             2740 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Knobbe, Martens, Olson and Bear
620 Newport Center Blvd. 16th Floor
                                                                                                                                                                                                                                                                           619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                          Conservative
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                                                                                                                                                                   linear
                                                                                                                                                                                single
                                                                         74.0%;
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COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
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                                                                           Score 14.8;
Pred. No. 51;
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Pred. No. 5:
                                                          Mismatches
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                                                                                         DB 1;
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                                                                                         Length 2740;
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                                                            Indels
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; LOCATION: 1.2740
; OTHER INFORMATION: /label= Hum_prosaposin
US-06-232-513A-5
                                                                                                                                                                                                                                                                                                               US-08-484-594A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local s
Matches 16
                                                                                                                                                                                                                                                                     Sequence 4, Application US/08484594A Patent No. 5714459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 9-U
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: /619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 08/100,247

FILING DATE: 30-JUL-1993

ATTORNEY/AGENT INFORMATION:
                                                                    NUMBER OF SEQUENCES: 11
CORRESPONDENCE & ADDRESS:
ADDRESSEE; Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                           1194 TCACGTGACTCAGCCAAA 1211
COMPUTER READABLE FORM:
                                                                                                                                                                     APPLICANT: O'Erien, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
TITLE OF INVENTION: DERIVED THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'Brien, John S.
TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
TITLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                2 tcacgtgacacagtcaaa 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%;
Local Similarity 88.9%;
es 16; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/232,513A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                    92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Campbell & Flores LLP
T: 4370 La Jolla Village Drive, Suite 700
San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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298 ACGGGACACNGTCAAAC 282

4 acgtgacacagtcaaac 20

Query Match Best Local S

Similarity

72.0%, 88.2%;

Score 14.4; Pred. No. 65;

DB 4;

Length 448;

Mismatches

0; Gaps

0

Conservative

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NAME/KEY: unsure LOCATION: (various positions within the sequence) LOCATION: (various positions within the sequence) OTHER INFORMATION: applicants are uncertain of bases designated as "n" US-09-060-756-666
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                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 666
SEQ ID NO 666
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 666, Application US/09060756 Patent No. 6183957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA FILE REPERENCE; 3495-0169
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gordon, Stephen APPLICANT: Billault, Alain
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                   ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                               TYPE: DNA
                                                                                                                                                 LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1194 TCACGTGACTCAGCCAAA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2740 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Israelsen, Ned A REGISTATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: MYTELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 30-0UL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
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EM: DOS
LSEQ for Windows Version
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US-08-645-641-145/c
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                                                                                             Sequence 145, Application US/08645641 Patent No. 5719032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 145, Application US/08053131 Patent No. 5661016
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/810,279
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY_AGENT INFORMATION:
NAME: Smith, William M.
REFIGENCEYDOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-326-2440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO: 145:
        APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
                                                         APPLICANT: Lonberg, Nils APPLICANT: Kay, Robert M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 16-DEC-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                        1 gtcacgtgacacagtcaaa 19
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36 GTCACGTTAACCAGTCAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                           Match 71.0%;
Local Similarity 84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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California
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                                                                                                                                                                                                                                                                                                                                        Score 14.2;
Pred. No. 66
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RESULT 15
US-07-83-408B-145/c
; Sequence 145, Application US/07853408B
; Patent No. 5799650
; Patent No. 5799670;
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Best Local Similarity
Watches 16; Conserve
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                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 07/904
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMITT, WILLIAM M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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MEDIUM TYPE: Flopy disk
COMPUTER: IHM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                APPLICANT: Lonberg, Nils.
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
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SOFTWARE: Patenti
                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
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                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                             ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-MAY-1996
                                                                                                                                                                                                        ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gtcacgtgacacagtcaaa 19
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                                                                                                                                                                                                                                         San Francisco
: California
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                                                                                                                                                                                                                         USA
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E: DNA (genomic)
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84.2%;
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pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
RELEPHONE: 415-326-2402
INPORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
RYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
NUCLEIC ACID
ROPOLOGY: linear
NUMBER: 16, Cansel (genomic)
US-07-853-408B-145

US-07-853-408B-145

US-07-853-408B-145

US-07-853-408B-145

US-07-853-408B-145

Ouery Match
Best Local Similarity 84.2%; Pred. No. 66;
Best Local Similarity 84.2%; Pred. No. 66;
Best Local Similarity 84.2%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 16; Conservative 0; Mis
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Title:
Perfect score:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 737)
11 (bases 1 to 737)
14 HoC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                       mRNA sequence.
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Tissue Procurement: Glibert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
plate: LLAM8543 row: c_column: 13
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                         Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Lu29"
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/strain-"CZECH II (feral)"
/db_xref-"taxon:10090"
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Pred. No. 31;
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                                                                                                                                        Rattus sp.
                                                                                                                                                                                                                                              AII04756 295 bp mRNA EST EST214045 Normalized rat heatt, Bento Soares Rattus sp. cDNA clone RHECI50 3' end, mRNA sequence.
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninol P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                  AI104756.1
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Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uRL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishlyama,Y., Westover
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                                             (bases 1 to 295)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by captrapper, cDNA went through one round of normalization to Rot - 20,0 and subtraction to Rot - 459.0. Second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="B230316K05"
/clone=lib="RIKEN full-length enriched, adult male corpora
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/db_xref-"taxon:10090"
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/dev_stage="adult"
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43 c
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94.7%;
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                                                                                        Chordata;
Rodentia;
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Pred. No. 89;
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Sciurognathi; Muridae; Murinae;
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                      Quackenbush, J.,
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В

/db\_xref="taxon:10090" /clone="RPCI-23-289M15"

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FEATURES
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AUTHORS
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                                                                                                               Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library avaliability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 289 row: M column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ015172 438 bp DNA bos Ar Ever AZ015172 A289M15.TJ RPCI-23 Mus musculus genomic clone RPCI-23-289M15
                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                              Class: BAC ends.
                                                                                                                                                                                                                                                                          Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Other_GSSs: RPCI-23-289M15.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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AZ015172
AZ015172.1 GI:7090556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
Contact: Lee, NH
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                                                                                               Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Normalized rat heart, Bento
/note="Organ: heart; Vector: pT7T3Pac;
Site_2: Not!"
a 49 c 74 g 85 t
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/db_xref-"ATCC (inhost):2025643"
/db_xref-"taxon:10118"
/clone-"RHECI60"
/organism="Mus musculus"
/strain="C57BL/6J"
                                                       Location/Qualifiers
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94.7%;
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Pred. No. 92;
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HS_3158_A1_H09_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3158 Col=17 Row=O, DNA sequence.
A0798101
                                                                                                                                                                                                                                                                                                                                                                            Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@t.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 3158 row: 0 column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahairas,G.G., Waliace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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h 87.0%;
Similarity 94.7%;
18; Conservative
                                                                                                                                                                                                                                                                                                High quality sequence stop: 482.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         Seg primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                         176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
/lab_host="DH10B"
                                                                                                                     /note="organ: sperm; Vector: pBeloBAC11; BAC Clones
E-Coli DH10B"
78 c 78 g 149 t 1 others
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                                                                                                                                                                                               /clone_"Plate-3158 Col-17 Row-O"
/clone_11b-"CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                           /organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                             /sex-"male"
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94.7%;
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      Score 17.4; D
Pred. No. 98;
O; Mismatches
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Pred. No. 97;
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                                                                           AUTHORS
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VERSION
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                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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EST223932 Normalized
RSPCR68 3' end, mRNA
Takifugu rubripes.

Takifugu rubripes.

Takifugu rubripes

Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;

Rotinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu:

1 (bases 1 to 258)

Elgar,G.; Clark,M.S.; Smith,S.; Meek,S.; Warner,S.; Edwards,Y.J.K.;

Unrania,Y.; Williams,G. and Brenner,S.

Direct Submission, Cambridge, CB10 15B. UK Email:

Centre, Hinxton, Cambridge, CB10 15B. UK Email:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                             FR0039113 258 bp DNA GSS 22-OCT-19: Fugu rubripes GSS sequence, clone 090H03dE7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The institute for Genomic Research 9712, Medical Center Drive, Rockville, 9712 (301)-838-3529
Fax: (301)-838-0528
Email: nhleedtigr.org
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
On Oct 8, 1998 this sequence version
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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                                                                                                                                                                                                                                    GSS; genome survey sequence
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/clone="RSPCR68"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site_1: E
Site_2: Not1"
a 101 c 87 g 142 t
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94.7%;
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                                            296
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                                       GTCACATGACACAGTCAACC 277
                                                                    gtcacgtgacacagtcaaac 20
                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                          Submitted (11-OCT-1999) MRC Human Genome Mapping Centre, Hinxton, Cambridge, CB10 ISB. UK Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS; genome survey sequence
Takifugu rubripes.
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

1 (bases 1 to 400)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                              One pass dye-terminator sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One pass dye-terminator sequencing of cosmid cloned genomic sequence.
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PRIMER: KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submission
                                                                                                                                                                                      /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 090H03"
/clone="090H03FD3"
/clone="090H03FD3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_11b="cosmid 090H03"
/clone="090H034E7"
66 c 58 g 64 t
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                                                                                                             90.0%;
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                                                                                                             Score 16.8; DB 222;
Pred. No. 2e+02;
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Pred. No. 1.9e+02;
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ORGANISM
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VERSION
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                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musines; Misses 1 to 539)

1 (bases 1 to 539)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCACATGACACAGTCAACC
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        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM8759 row: b column: 24 High quality sequence stop: 536.
                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BE368176
                                                                                                                                                                                                                                                                                                                                                                                                      BE368176 539 bp mRNA EST 21-JUL-2000 601222089F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3590711 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 90.0
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/clone="090H03cA5"
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/db_xref="taxon:31033"
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pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF500440 548 bp mRNA EST 16-APR-2001 AT15369.5prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster cDNA clone AT15369 5 similar to CG9778:
                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 548)
                                                                                                                                                                                                                                                                                                                            hit genomic sequence AE003606
Plate: AT.153 row: F column: 9
High quality sequence stop: 513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley Drosophila Gene Collection Project Unpublished (2000)
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Eukaryota; Metazoa; Arti
                                                                                                                                                                                                                                                                                                                                                                                         Email: http://www.fruitfly.org/EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type-"spontaneous tumor, metastatic to mammary. Stem cell origin." \label{eq:total_total}
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                                                                                                                  /dev_stage="0-3 day old Ore-R males"
/lab_host="plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib-"NCI_CGAP_Lu29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3590711"
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                                    /note="Organ: ADULT testes; Vector: pOTB7; Site_1: ECORI; Site_2: Xho1; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'lab_host="DH108"
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                   Margaret Fuller, Sized fractionated cDNAs were directly
                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                      /clone_lib="AT Drosophila melanogaster adult testes pOTB7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "", Clark,N., Dubuque,T., Elliston,R., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merrk EST project
Unpublished (1955)
Contact: Wilcon,
                         al Similarity
18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zd53e10.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 63
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: ETPrimer
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1 155 c 152 g 126 t
                                                                                                                                                                                                              same fetus as the fetal lung library, Soares fetal lung NbHL19W."

150 c 147 g 143 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Homo sapiens"
/db_xref="GDB:1269769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:344394"
                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                               90.0%;
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Pred. No. 2
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                                Score 16.8; DB 190; Length 562;
Pred. No. 2.1e+02;
0; Mismatches 2; Indels 0;
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COMMENT

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FEATURES

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DEFINITION

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Matches Query Match

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9435 row: i column: 05
High quality sequence stop: 657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (Dases 1 to 804) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Inc.
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Tetraodon nigroviridis genome survey sequence T7 end of clone
135P15 of library G from Tetraodon nigroviridis, genomic surve
                                                                                                                                                        AL195730.1 GI:7833880
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/clone_lib-"NCI_CGAP_Li9"
/lab_host-"DH10B (T1 phage-resistant)"
/note-"Organ: liver; Vector: pCRV'SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 216 c 233 g 159 t
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Roest-Crollius, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS03EDV 835 bp DNA GSS 17-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of civ
020G19 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12 APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lay scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Bernot,A., Fizames,C., Wincker,P., Brottler Saurin,W. and Weissenbach,J.
                                                                                                                                                                                Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                      Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                               Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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/db_xref="taxon:99883"
/clone="135P15"
/clone="15"6"
/note="Genoscope sequence ID : COAG1:
/note="Genoscope 246 g 200 t 2 ot
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Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
SOURCE

/organism-"Tetraodon nigroviridis"
/db_xref-"taxon:99883"
/clone=10b-"G"
/note="Genoscope sequence ID : COBGO20AbIOSP1-end :
PUC-Or1"

BASE COUNT

185 a 245 c 233 g 168 t 4 others
ORIGIN

Ouery Match
Best Local Similarity 90.0%; pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Search completed: July 25, 2001, 04:54:54

Search completed: July 25, 2001, 04:54:54

Job time: 10427 sec
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Title:
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Variability at the uridine diphosphate glucuronosyltransferase 1A1
Promoter in human populations and primates
Pharmacogenetics (1999) In press
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Pongo pygmaeus UDP-glucuronosyltransferase lAl (UGT1A1) gene,
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E. 57th Street, Chicago, IL 60637, USA
Location/Qualifiers
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Ybazeta,G., Hall,D. and Di Rienzo,A.
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Hall,D.; Ybazeta,G.; Destro-Bisol,G.; Petzl-Erler,M.L. and Di
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/protein_id="AAF09176.1"
/db_xref="GI:6456548"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UDP-glucuronosyltransferase 1A1" <91. >177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Gorilla gorilla"
/db_xref-"taxon:9593"
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tive 0;
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(UGT1A1) gene,
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Cebus apella UDP-glucuronosyltransferase
promoter region and partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission submitted (18-MAR-1999) Human Genetics, University of Chicago, 924 E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 200)
Ybazeta,G., Hall,D. and Di Rienzo,A.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus. 1 (bases 1 to 207)
                                                                                                                                                                                                           Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA Location/Qualiflers
                                                                                                                                                                                                                                                                                       variability at the uridine diphosphate glucuronosyltransferase IA1 promoter in human populations and primates pharmacogenetics (1999) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                      AF135470.1 GI:6456557
                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                             Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                                                                 Rienzo, A
                                                                                                                                                                                                                                                                                                                                             Hall,D., Ybazeta,G.,
                                                                                                                                                                                                                                                                                                                                                                                                Cebus apella
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                                                                                        /gene-"UGT1A1"
144. .>207
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/protein_id="AAF09177.1"
/db_xref="GI:6456550"
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/db_xref="taxon:9600"
                    /product="UDP-jucuronosyltransferase 1A1"
/protein_id="AAF09181.1"
/db_xref="GT:6456558"
                                                                                                                    ^144.
                                                                                                                                                                    /organism="Cebus apella"
/db_xref="taxon:9515"
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        /translation="MPACPGPAAVCAGPGSVPCWE"
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                                                                            /gene="UGT1A1"
                                                                                                                  /product="UDP-glucuronosyltransferase 1A1" <144. .>207
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                                                                                                                                                               1 tttgctcctgccagaggtt 19
                                                                                                                                  TTTGCTCCTGCCAGAGGTT 108
                                                                                                                                                                                          ch 100.0%; 1 Similarity 100.0%; 19; Conservative 0
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Gorilla gorilla
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AF135471 208 bp DNA PRI 21-NOV-1999 Saimiri boliviensis UDP-glucuronosyltransferase 1A1 (UGT1A1) promoter region and partial Cds.
AF135471
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1 (bases 1 to 208)
Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Direct Submission
Submitted (18-MAR-1999) Human Genetics,
Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variability at the uridine diphosphate glucuronosyltransferase 1A1
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Ybazeta, G., Hall, D. and Di Rienzo, A.
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                                                                                                                                                                                                                                                                                            /product-"UDP-glucuronosyltransferase lAl"
/protein_id-"AAF09175.1"
/protein_id-"AAF09175.1"
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/TANSlation="MAVESOGGHPLVLGLLLCVLGPVVS"
47 c 62 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                             /gene="UGT1A1"
133. .>208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="from Yerkes Regional
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/db_xref="taxon:9593"
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Pred. No.
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(UGT1A1) gene,
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                                                                                                                          JOURNAL
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KEYWORDS
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AF135462/c
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tes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rienzo,A. Variability at the uridine diphosphate glucuronosyltransferase IAI promoter in human populations and primates Pharmacogenetics (1999) In press
                                                                  Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                         promoter in human populations and Pharmacogenetics (1999) In press 2 (bases 1 to 234)
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 234)
                                                                                                                                                                                                                                                                                                               Pan
                                                                                                                                                                                                                                                                                                                                                                                   promoter region and partial AF135462
                                                                                                                                                                                                                                                                                                                                                                                                                  AF135462 234 bp DNA PRI 21-NOV-1999 Pan paniscus UDP-glucuronosyltransferase 1A1 (UGT1A1) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-MAR-1999) Human Genetics, University of Chicago, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 208) Ybazeta, G., Hall, D. and Di Rienzo, A.
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                                                                                                                      Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                Variability at the uridine diphosphate glucuronosyltransferase 1A1
                                                                                                                                                                                                                     Rienzo, A.
                                                                                                                                                                                                                                    Hall, D., Ybazeta, G., Destro-Bisol, G., Petzl-Erler, M.L. and Di
                                                                                                                                                                                                                                                                                                                          pygmy chimpanzee.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolivian squirrel monkey.
                                                                                                            rect Submission
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                                                                                                                                                                                                                                                                                                           paniscus
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/organism="Pan paniscus"
/db_xref="taxon:9597"
                                                 Location/Qualifiers
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52 c 58 g 54 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="UDP-glucuronosyltransferase 1A1"
/protein_id="AAF09182.1"
/db_xref="GI:6456560"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Saimiri boliviensis"
/db_xref-"taxon:27679"
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                                                                                       University of Chicago,
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ORGANISM
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AF135463/c
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              Query Match
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 l Similarity
19; Conserv
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AF135463.1 GI:6456543
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                  Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
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100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                     /translation="mavesoggrpLvLGLLLCVLGPVVSHAGK"
53 c 69 g 62 t
                                                                                                                    /codon_start=1
/product="UDP-glucuronosyltransferase 1A1"
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/db_xref="GI:6456544"
                                                                                                                                                                                                                                                                                       /organism-"Pan troglodytes"
/db_xref-"taxon:9598"
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                                                                                                                                                                                                                              /product="UDP-glucuronosyltransferase 1A1"
<148. .>234
                                                                                                                                                                                                                                                           /gene-"UGT1A1"
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                                                                                                                                                                                /gene-"UGT1A1"
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            Score 19;
Pred. No.
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15;
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   0;
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                               Length 234;
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1A1 (UGT1A1) gene,
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141 TTTGCTCCTGCCAGAGGTT 123

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VERSION
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AF357220/c
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                                 74 Triecrecreccheagerr 56
                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-MAR-2001) Medicine/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th Street, Augusta, GA 30912, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of TATA box TA repeat region [6(TA)repeat] of human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in an African American individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF357220
AF357220.1 GI:13448828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McKle, K., Addington, T., Nguyen, T.S., Glendenning, M., Kutlar, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kutlar,A.
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                                                                                                                        Similarity
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                                                                                                    Conservative
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                                                                                                                                                                                         /codon_start=1
/codon_start=1
/product="bilirubin UDP-glucuronosyltransferase 1"
/protein_id="NAK27223.1"
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GAIQCLQRCHEIVVLAPDASLYIRDG"
69 c 95 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="UGT1"
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                                                                                                                      100.0%;
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                                                                                                                     Score 19;
Pred. No. 1
                                                                                                    Mismatches
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等人的 我就成了你是一切,好你会也我们好好的人

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AUTHORS
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327 TITGCTCCTGCCAGAGGTT 309
                                                                  y match 100.0%; Score 19; DB Local Similarity 100.0%; Pred. No. 14; hes 19; Conservative 0; Mismatches
                      1 tttgctcctgccagaggtt 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 531)

McKie, K., Kutlar, F., Glendenning, M. and Kutlar, A.

7(TA) repeat polymorphism of the TATA box of human bilirubin

UDP-glucuronosyltransferase 1-[UGTIA1*1) gene in a patient with

sickle cell anemia + high bilirubinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 531)
MCK1e,K., Kutlar,F., Glendenning,M. and Kutlar,A.
Direct Submission
Submitted (23-FEB-2001) Medicine/Hemoglobin DNA Laboratory, Medical
College of Georgia, 15th St., AC-1000, Augusta, GA 30912, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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279. .
                                                                                                                                                                                  GAIQQLQQRGHEIVVLAPDASL"
121 c 137 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="repeat polymorphism compared to UGTIA1 sequence presented in GenBank Accession Number AF180372; contains 7 ta repeats frequently detected in patients with high bilirubinemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"UGT1A1"
279. .>292
                                                                                                                                                                                                                      db_xref="gI:13569709"
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
                                                                                                                                                                                                                                                          /product="bilirubin UDP-glucronosyltrasferase 1-1"
/protein_id="AAK31204.1"
                                                                                                                                                                                                                                                                                                                                                                /gene-"UGT1A1"
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/rpt_unit=ta
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/tissue_type="blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                            codon_start=
                                                                                                                                                                                                                                                                                                                 'gene-"UGTlA1"
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 323
                                                                          Local
                   1 tttgctcctgccagaggtt 19
 TTTGCTCCTGCCAGAGGTT 305
                                                          1 Similarity
19; Conserv
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Kutlar.F., Sromek.E., Leithner.C., Nechtman.J. and Kutlar.A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF180372 541 bp DNA PRI 05-OCT-1999
Homo sapiens bilirubin UDP-glucuronosyltransferase 1-1 (UCT1) gene,
UCT1*1 aliele, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-AUG-1999) Medicine, He Center, Medical College of Georgia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 541)
Kutlar, F., Sromek, E., Leithner, C., Nechtman, J. and Kutlar, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sickle cell anemia Unpublished
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                                                                                                                                                 123
                                                          Conservative
                                                                                                                                              GAIQQLQQRGHEIVVLAPDASLYIRDG"
124 c 141 g 153 t
                                                                                                                                                                      /product-"bilirubin UDP-glucuronosyltransferase 1-1"
/protein_id-"AAF01205.1"
/db_xref-"GI:6010650"
/translation="MAYESOGGRPLVIGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                          'note-"polymorphic region"
'rpt_type-tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="UGT1"
'note="GNT1; UGT1A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome="2"
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                                                                                                                                                                                                                                'note="UDP glycosyltransferase 1"
'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="UGT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'allele="UGT1*1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="whole blood"
                                                                                                                                                                                                                                                                                                                                    ote "Ritter, J.K., 7:3257-3261"
                                                                                                                                                                                                                                                                                           roduct="bilirubin UDP-glucuronosyltransferase 1-1"
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Pred. No. 14;
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                                                                                        89;
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                                                                                       Length 541;
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605 TTTGCTCCTGCCAGAGGTT
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Sequence 5 from Patent W09732042.
A65504
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Homo sapiens chromosome 2 UDP-glucuronosyltransferase
gene, UGTIA1*33 allele, partial cds.
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1 (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-DEC-1998) Center Massachusetts Avenue, E17-540, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guillemette, C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 918)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
127 c 151 g 18
                                     /translation="mavesqggrplylglllcvlgpyvshagkillipydgshwlsml
gaiqqlqqrgheivylapdaslyirdgafytlktypyppqrsdykssfysgghnyfen
DSFLQRVIKTYKKIKKDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIV
                                                                                                 /product="UDP-glucuronosyltransferase"
/protein_id="AAG43197.1"
/db_xref="GI:12002135"
                                                                                                                                                                                                        ....e="22...918; lAl variant allele; L233R"
/allele="UGTIA1*33"
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AOYLSLDTVEFLHALDCSLEFEATQCDNDFSYVPRDLSSHSDHMTFLQRVKNMLIAFS
QNFLCDVVYSPYATRASEFLQREVTVQDLLSSASVMLFRSDFVKDYPRPIMFNMVFVG
                                                                                                                                                                                                                                                                                                               /gene="UGT1A1"
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/db_xref="taxon:9606"
                                                                                                                                                                               'gene="UGT1A1"
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                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                             product="UDP-glucuronosyltransferase"
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Cambridge, MA 02139, USA
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ase (UGT1A1)
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bilirubin UDP-glucuronosyltransferase; isozyme.
Homo sapiens (tissue library: cosmid) liver DNA.
Homo sapiens
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Human bilirubin UDP-glucuronosyltransferase (UGTIA) gene isozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel complex locus UGT1 encodes human bilirubin, phenol, and other UDP-glucuronosyltransferase isozymes with identical carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ritter,J.K., Crawford,J.M. and Owens,I.S. Cloning of two human liver bilizubin UDP-glucuronosyltransferase CDNAs with expression in COS-1 cells J. Biol. Chem. 266 (2), 1043-1047 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ritter, J.K., Chen, F., Sheen, Y.Y., Tran, H.M., Kimura, S., Yeatman, M.T. and Owens, I.S.
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Mammalia; Eutheria; Primales; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter region and partial D87674
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttgctcctgccagaggtt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:*
                                                                                                                                                                                                                                                       Length
                    1167
1167
1167
1207
12095
1156
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                                                                                                                                                                                                                                                       DB
                                                                         AAT79540
AAT79540
AAQ33024
AAZ45058
AAZ45074
AAF75200
AAZ16518
AAV222955
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                                                                                                                                                                                                                                                                                                                SUMMARIES
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                  Human gene express
cDNA encoding huma
Nucleotide sequenc
Human nodal protei
Human transport pr
                                                                                                               UGT1*1 gene exon 1
Upstream DNA seque
UGT1A Exon 1 from
Forward PCR primer
Forward PCR primer
Human 2hdeltalp DN
                                                                                                                                                                                                                                                       Description
WE CHATTER CONTRACTOR
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Human Low adenosin	AAF21105	21	30	77.9	4		O
Genomic iragment	AAF28535	22			4		a
CONA encoding con	AAX85766	20			4	43	
Cobra CVF1 coding	AAQ77790	15			4		
Human ORFX	AAC75767	21			4		o
sequen	AAZ87998	21		77.9	•		o
$\sigma$	AAV32554	19			4	39	
E-Z ligan	AAV18619	19			4	38	
Human TIE-2 ligand	AAT14650	17			•	37	
Human TIE-2 ligand	AAT44321	17			4	36	
Human angiopoietin	AAZ92215	21			4	<u>ა</u>	
Human angiopoietin	AAZ92213	21			4	ω A	
Human angiopoietin	AAC67774	21			4	ω	
Nucleotide sequenc	AAV18614	19			4	3 2	
	AAV18613	19			4	3	
	AAC99839	21	800	77.9	4	30	o
Human prostate	AAZ33534	20	697	77.9	٠	29	
Human breast c	AAA57279	21	530	77.9	•	28	a
Human	AAZ80032	21	508	77.9	•	27	O
Human	AAV02162	18	479	77.9	•	26	
Partial CDNA Cione	AAT88072	18	479	77.9	•	25	
. 17	AAC56976	21	471	77.9	*	24	Ω
radiata	AAC57049	21	469	77.9	*	23	a
radiata	AAC57046	21	430	77.9		22	o.
secreted	AAX40904	20	405		14.8	21	
	AAC03243	21	404	77.9	*	20	
	AAC01025	21		77.9		19	
	AAC57038	21		77.9		18	O
radiata	AAC57066	21		77.9		17	a
lum venen	AAF10976	21		77.9		16	a
Arabidopsis thalla	AAC47622	21		83.2	٠.	15	
Sheep mammary glan	AAT10554	17		83.2	٠.	<u>1</u> 4	
	AAV22956	19		83.2	٠.	ω	O
Human pancreatic c	AAC98907	21		83.2		12	O

## ALIGNMENTS

RESULT	
ID AAT	AAT79544 standard; DNA; 19 BP.
XX	
AC	AAT79544;
Z X	23-JAN-1998 (first entry)
×	
DE	UGT1*1 gene exon 1 upstream PCR primer U.
XX	Uridine diphosphate glucuronosyltransferase gene; UCT;
XX	Gilbert's syndrome; GS; unconjugated hyperbilirubinaemia;
XX.	bilirubin glucuronidation; Crigler-Najjar; type 2; drug mecaportsm;
XX	Drug trial efficiency; screening; FCK primer; 33.
8 8	Synthetic.
XX	
y PN	W09732042-A2.
PD	04-SEP-1997.
PF XX	03-MAR-1997; 97WO-GB00577.
g X	16-MAR-1996: 96GB-0005598.
PR	
₽ ×	(UYDU-) UNIV DUNDEE.
P X	Burchell B;
S X	WPI: 1997-448702/41
23 X	Improving drug trial efficiency comprises identifying participants

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をおけるというでは、人間はは、これが必要が、これが、一般を表している。 は、我们では一般の意思をいったからできます。 しばれば 教育

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TANDER OF THE TRANSPORT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            рЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with reduced bilirubin glucuronidation capacity. Analysis of the genetic basis of GS has allowed 2 forms to be identified. One is a mild form associated with a homozygous 2 bp insertion in the TNTA sequence upstream of the UGTI*1 exon 1, and the other is a more severe form associated with heterozygosity for a mutation which, when homozygous, causes Crigar-Najjar type 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on basis of them possessing.
                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uridine diphosphate glucuronosyltransferase gene; UGT; Glibert's syndrome; GS; unconjugated hyperbilirubinaemia; bilirubin glucuronidation; Crigler-Najjar; type 2; drug metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Upstream DNA sequence of UGT1*1 gene exon 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trial efficiency; screening; ss
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317..324
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/note= "SP1 binding site"
180..191
/note= "feature indicated in patent, but no further
explanation is given"
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Qy

1 tttgctcctgccagaggtt 19

Matches

19;

Conservative

0:

Mismatches

0

Indels

0

Gaps

0

Query Match
Best Local Similarity

100.0%;

Score 19; Pred. No.

N DB 2.2; 18;

Sequence 620

BP; 157 A; 127 C; 151 G;

185 T; 0 other;

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capacity. Analysis of the genetic basis of GS has allowed 2 forms to be capacity. Analysis of the genetic basis of GS has allowed 2 forms to be dentified. One is a mild form associated with a homozygous 2 bp insertion in the TATA sequence upstream of the UGT1*1 exon 1, and the other is a more severe form associated with heterozygosity for a mutation which, when homozygous, causes Crigler-Najjar type 2 disease. The first form is autosomal recessive and the second is inherited dominantly. Patients suffering from GS, which is benign, may have altered metabolism of some drugs, making it difficult to determine if an effect is due to the drug or the syndrome. Drug trial efficiency would be improved if potential participants can be screened for the genetic basis of GS, and eliminated or included on basis of them possessing or not possessing GS. In this case, screening involves PCR amplification of the UGT gene, using the primers described in AAT79541-44.
                                                                                                                                                                                                                 This sequence represents the upstream sequence, positions -611 to 9 in the patent, of uridine diphosphate glucuronosyltransferase (UGT) gene 1*1 exon 1. This gene is known to be associated with filbert's syndrome (GS). GS is a mild, common form of unconjugated syndrome (GS). GS is a mild, common form of unconjugated by the syndrome (GS).
                                                                                                                                                                                                                                                                                                                                   Improving drug trial efficiency comprises identifying participants with Gilbert's syndrome - useful as their altered drug metabolism may hinder result interpretation
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(2) Exon 2, represented in AAQ33025;
(3) Exon 3, represented in AAQ33026;
(4) Exon 4, represented in AAQ33026;
(5) Exon 5, represented in AAQ33026;
(6) Exon 5, represented in AAQ33027; and
(6) About 69 kb. of non-sequenced DNA.

Six unique N-termini of 286-289 amino acids are encoded by
six different first exons and identical C-termini of 246 amino
acids are encoded by the common exons 3-5. The UGT1 gene locus
encodes a family of UDP-glucuronosyl transferase isozymes, two of
which metabolise bilirubin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ33024 standard; DNA; 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                             The isolated gene locus, UGT1, has a sequence of about 10000 bp which represent (1) Exon 1, comprising 6 transcriptional units (UGT1F, E, D, C, BP and A), represented in AAQ27368 and
                                                                                                                                                                                                                                                                                                      Isolated gene locus UGT1, DNA segments and diagnostic probes for diagnosing Gilbert's disease and Crigler-Najjar syndrome types I and II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UGTIA; UGTIBP; UGTIC; UGTID; UGTIE; UGTIF; isozyme; bilirubin;
UDP-glucuronosyl transferase; CN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UGT1A Exon 1 from the UGT1 gene locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ33024;
                                                                                                                                                                                                                                                                      Disclosure; Fig 1F; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Owens IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09212987-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                (UGT1F, E, D, C, BP and A
AAQ33020-24 respectively;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR30194.
                                                                                                                                                                                                                                                                                                                                                                                              1992-284593/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ritter JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0639453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-US00282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "representation of 5 kbp of
non-sequenced DNA between the sequences
represented in AAQ33024 and AAQ33025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/note= "encodes transferase isoform; see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66..909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= c
label= UGT1A_Exon_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *representation of 11.7 kbp of non-sequenced DNA between the sequences represented in AAQ33023 and AAQ33024*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ45058/c
cc alcohols, amines and fatty acids. Many of the reactions catalysed by CC UGTs result in toxic substances being converted to compounds which are come water soluble and are excreted. The invention relates to and identifies UGT1 polymorphisms (ARAZ5004-Z45041). The polymorphisms CC sequences are useful as probes for detecting UGT1 locus polymorphisms, CC indicative of altered UGT1 expression or activity. These polymorphisms CC indicative of altered UGT1 expression or activity. These polymorphisms CC are associated with CT19ler-Nejjar and Gilbert syndromes (unconjugated CC hyperbilirubinaemia) and drug metabolism. The genotyping of the UGT1 gene CC is used to predict the rate of metabolism of UGT1 substrates, possible CC dosage), and to screen for diseases caused by exposure to toxins and to sequences, including polymorphisms, can also be used to produce the CC corresponding protein/corits fragments) or to generate transgenic corresponding protein/corits fragments) or to generate transgenic collaborations of modified cells e.g. for pharmacogenetic screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucuronic acid, Crigler-Najjar syndrome; Gilbert syndrome; jaundice; unconjugated hyperbilirubinaemia; drug metabolism; transgenic animal; pharmacogenetic screening; diagnose; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1167 BP; 255 A; 259 C; 272 G; 340 T;
                                                                                                                                                                                                                                                                                                                                                      diphosphate-glucuronosyltransferase 1 (UGT1) exon sequences. The UGTs are a family of enzymes that catalyse the glucuronic acid conjugation of a wide range of endogenous and exogenous substrates including phenois.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ45058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ45058 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Page 16; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid representing polymorphisms in diphosphate glucuronosyltransferase gene, used evaluation of drug metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-052981/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penny L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09957322-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forward PCR primer used in the secondary amplification of UGT1 exon 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primers AAZ45042-Z45073 are used to amplify human uridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 TIGCTCCTGCCAGAGGTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ttgctcctgccagaggtt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0084807
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the human uridine for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1167;
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S
    Sequence
    17
 BP; 5
A; 4 C; 6 G; 2 T; 0 other;
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В
                 S
                                    Matches
                                                    Query Match
16 TTTGCTCCTGCCAGAG 1
                                           Local Similarity
        1 tttgctcctgccagag 16
                                    15;
                                  Conservative
                                       84.2%; Score 16;
100.0%; Pred. No.
                                  0
                                                 DB 21; Length 17;
                                         5
                                 0
                                0
                               Gaps
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0

QY

1 tttgctcctgccagag 16

Matches Query Match

16;

Conservative

0

Mismatches

0

Indels

0

Gaps

0

Similarity

100.0%;

84.2%;

Score 16; Pred. No.

DB 21; Length 17;

ΒP

Forward PCR primer for sequencing UGT1 exon 1A polymorphism #1

Uridine diphosphate-glucuronosyltransferase 1; UGT1; polymorphism; probe; glucuronic acid: Crigler-Najjar syndrome; Gilbert syndrome; Jaundice; unconjugated hyperblirubinaemia; drug metabolism; transgenic animal; screening; diagnose; PCR primer; ss.

New nucleic acid representing polymorphisms in the human uridine diphosphate glucuronosyltransferase gane, used for diagnosis and evaluation of drug metabolism

Examples; Page 19; 63pp; English.

The polymorphisms sequences are useful as probes for detecting UGT1 locus polymorphisms, indicative of altered UGT1 expression or activity. These polymorphisms are associated with Crigler-Najdar and Gilbert syndromes (unconjugated hyperbilirubinaemia) and drug metabolism. The genotyping of the UGT1 gene is used to predict the rate of metabolism of UGT1 substrates, possible drug-drug interactions and adverse side effects (i.e. to optimize drug dosage), and to screen for diseases caused by exposure to toxins and to study the effects of polymorphisms on enzymatic activity. The UGT1 sequences, including polymorphisms, can also be used to produce the corresponding protein (or its fragments) or to generate transgenic animals or modified cells e.g. for pharmacogenetic Primers AAZ45074-Z45109 are used to sequence the human uridine diphosphate-glucuronosyltransferase 1 (UGT1) exon polymorphism sequences. The UGTs are a family of enzymes that catalyse the glucuronic acid conjugation of a wide range of endogenous and exogenous substrates including phenols, alcohols, amines and fatty acids. Many of the reactions catalysed by UGTs result in toxic substances being converted to compounds which are more water soluble and are excreted. The invention relates to and identifies UGT1 polymorphisms (AAZ45004-Z45041).

Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 other

EXEXEXEX EXXXXX

12-OCT-1999

(first entry)

Human; gene; gene expression product; diagnosis; therapy; probe;

Human gene expression product cDNA sequence SEQ ID NO:3988

AAZ16518/c

AAZ16518 standard; cDNA; 457 BP.

RESULT

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1119

GCTCCTGCCAGAGGTT 1104

Matches Query Match Best Local

Local Similarity nes 16; Conserv

Conservative

0;

Mismatches

100.0%;

Score 16; Pred. No.

DB 75;

22; 0

Length 1307; Indels

0;

Gaps

0;

4 gctcctgccagaggtt 19

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                                  The present invention relates to a novel Notch receptor ligand. The invention is useful for detecting Notch ligand expression in human cancer cells or melanoma cells. Also useful for enhancing angiogenesis in a mammal, useful when the mammal exhibits
Sequence 1307 Bp; 294 A; 328 C; 396 G; 289 T; 0 other;
                                                                                                   Disclosure; Fig 6; 66pp; English.
                                                                                                                         Novel notch receptor ligands useful for modulating angiogenesis and immune responses for treating rheumatoid arthritis, cancer-related angiogenesis to stop tumor growth, and as diagnostic reagents -
                                                                                                                                                                                 WPI; 2001-211201/21.
                                                                                                                                                                                                         Vivien C, Rohan M,
                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                              19-AUG-1999;
                                                                                                                                                                                                                                                                                      17-AUG-2000; 2000WO-US22609
                                                                                                                                                                                                                                                                                                                22-FEB-2001
                                                                                                                                                                                                                                                                                                                                        WO200112664-A2
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Notch receptor; ligand; cancer; melanoma; ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human 2hdeltalp DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2001 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF75200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF75200 standard; DNA; 1307 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGCTCCTGCCAGAG 1
                                                                                                                                                                                                                                                             99US-0149934
                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                           Williams LT;
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RESULT
AAV22955/
ID AAV2
XX
AC AAV2
XX
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                                                                                                                                                                                                                                                                                                                            The present invention describes a library of human polynucleotides comprising the sequences given in AAX12532 to AAX17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one cdifferentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one cof the 5248 polynucleotide sequences given in AAX12532 to AAX17779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, can be used for a variety of purpose, e.g. detection of expression levels, can be used for raising antibodies for experimental, diagnostic and comping, tissue typing or profiling, forensics, genetic analysis and construct can be used for raising antibodies for experimental, diagnostic and considered protein; and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to cancer). The polynucleotides or susceptibility to a disease such as cancer; The polynucleotides can also be used to screen for and lung cancer. The polynucleotides can also be used to screen for coptide analogues and annagement of colorectal cancer, breast cancer, cand lung cancer. The polynucleotides can also be used to screen for petide analogues and annagement of colorectal cancer.
                                                                                                                                                                                                            Query Match
Best Local S
Matches 17
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
           мү22955)
                                                 NAV22955 standard; cDNA; 843 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Glese K, Into
Jones WL, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Rei
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09938972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                               Sequence 457 BP; 120 A; 88 C; 93 G; 139 T; 17 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1892-1893; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                          300 TITGCTCCTCCCAGAGCTT 282
                                                                                                                                                              1 tttgctcctgccagaggtt 19
                                                                                                                                                                                                            l Similarity 89.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIRON CORP. HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US01619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0080666
                                                                                                                                                                                                                           83.2%;
                                                                                                                                                                                                            0;
                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                Mismatches
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No. 83
                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                               DB
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                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                               Length 457;
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AAV6866/G ID AAV68666 standard, DXA, 1095 BP. XX

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412 TCTGCTCCTGCGAGAGGTT 1 tttgctcctgccagaggtt 19 Conservative

394

Query Match Best Local Similarity

83.28;

0

Mismatches

'n

0

0

Score 15.8; 1 Pred. No. 89;

В

19; Length 843;

Matches

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The present sequence encodes a human bone morphogenetic protein-16 (C (BMP-16). Human BMP-16 is a homologue of a murine protein celled nodal, which is expressed in the mouse node during gastrulation. BMP-16 cDNA is consisted from a human genomic library screened with a probe derived from the nodal DNA sequence. The BMP-16 proteins can induce the formation of bone, cartilage or other connective tissue. They can be used for treating companies to the connective tissue defects, periodontal disease or healing of various types of tissues and wounds. They can also increase neuronal, astrocytic and glial cell survival and therefore be useful in curanglantation and treatment of conditions exhibiting a decrease in euronal survival and repair. They can also exhibit properties such as angiogenic, chemotactic and/or chemotatractant properties, and effects concells including induction of collagen synthesis, fibrosis, cold inferentiation responses, cell proliferative responses and responses convolving cell adhesion, migration and extracellular matrices. These corresponds the proteins potential agents for wound healing, correduction of fibrosis and reduction of scar tissue formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated bone morphogenetic protein-16 - used to develop products for inducing formation of bone, cartilage and other connective tissue, particularly for wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
Sequence 843 BP; 176 A; 241 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Pages 33-34; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW56477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-217262/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celeste AJ, Murray BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09812322-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone morphogenetic protein-16; BMP-16; murine protein; nodal; formation; bone; cartilage; treatment; wound healing; reduction; fibrosis; scar tissue formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding human bone morphogenetic protein-16 (BMP-16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC
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511..840
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1..510
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244 G; 182 T; 0 other;
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18-JUN-1999 (first entry)

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                                      AAX31924/c
ID AAX31924 standard; DNA; 1156 BP.
                                                                         RESULT
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
              AAX31924;
                                                                                                                                                                                                                                                Sequence 1095 BP; 231 A; 296 C; 312 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                           therapeutically. Antibodies or other specific binding agents, are used to detect recombinant proteins and fragments of the Tango nucleotide sequence can be used as probes or primers for detecting the Tango gene, specifically mRNA, in usual hybridisation or amplification assays. These assays are used for diagnosis of diseases associated with abnormal expression of Tango proteins, e.g. detecting mutations in the Tango gene. Fragments of the Tango nucleic acid sequence are also used for genetic mapping and chromosome identification, and as antisense, ribozyme or triplex forming therapeutics. Antibodies may also be used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence encoding the human Tango-78 protein used in the method of the invention. Host cells containing the Tango protein are used to produce recombinant proteins for raising antibodies. It is also used in identifying specific binding agents (including cognate receptors), which can be used to
                                                                                                                                                                                                                                                                                 anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human Tango-78, -79 and -81 proteins - useful for diagnosis and treatment of Tango-associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  determine amounts of recombinant protein in cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-153693/13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Tango-78; host cell; recombinant protein; antibody; receptor; specific binding agent; probe; primer; hybridisation; amplification; mutation; genatic mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the human Tango-78 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1999 (first entry)
                                                                                                                  801 TCTGCTCCTGCGAGAGGTT 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV68666;
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                                                                                                                                  1 tttgctcctgccagaggtt 19
                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Tango-78"
                                                                                                                                                                                        89.5%;
                                                                                                                                                                            0
                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                     Score 15.8;
                                                                                                                                                                             Mismatches
                                                                                                                                                                                          92;
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                                                                                                                                                                                                        20;
                                                                                                                                                                          2;
                                                                                                                                                                                                     Length 1095;
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                                                                                                                                                                        Gaps
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CC capacities including sexual development, pitultary hormone production, CC and the creation of bone and cartilage. The Nodal and Lefty polypeptides CC are useful for enhancing or enriching the growth and/or differentiation CC of specific cell populations, eg. embryonic cells or stem cells. They can be used to treat such conditions as osteoarthritis, osteoporosis, and CC other connective tissues and/or organs such as liver, lung, cardiac, CC pancreas, and kidney. Compositions containing nodal and lefty proteins CC may be useful for growth formation, for treating periodontal disease and CC for modulating haematopoiesis, wound healing and tissue repair. They can CC also be used for the treatment of tumours, cancers, interstitial lung CC disease, and any disregulation of the growth and differentiation patterns CC consuppression, immunity, authritis, leukaemia, lymphomas, CC immunosuppression, immunity, bumoral immunity, inflammatory bowel crepresents a DNA encoding a uponal polypeptide. The present sequence crepresents a DNA encoding, or infectious diseases. The present sequence crepresents a DNA encoding and under the ArCC decosit No. 209992 and/or
                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel human nodal and lefty proteins which are members of the TGF-beta family. The human nodal and lefty proteins may be involved in a developmental process such as the correct formation of various structures or in one or more post-developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 1A; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolate human Nodal and Lefty polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nodal protein; lefty protein; TGF-beta; sexual development; human; bone; pituitary; cartilage; osteoparthritis; osteoporosis; haematopolesis; periodontal disease; wound healing; tissue repair; tumour; cancer; interstitial lung disease; autoimmunity; leukaemia; lymphoma; immunity; immunosuppression; inflammatory bowel disease; myelosuppression;
                                                      the nodal protein is deposited under the ATCC deposit No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nodal protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0056565
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/product- "Nodal protein"
/note- "the start codon is not indicated"
517.849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "sequence coding for the active fragment of
the Nodal polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..852
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Query Match Best Local S Matches 17

1 Similarity 17; Conserv

Conservative

0

89.5%;

Score 15.8; Pred. No. 93 Mismatches

DB 20; Ņ

Length 1156; Indels

0 Gaps

0;

Sequence 1156 BP;

285 A; 298 C;

340 G;

233 T;

0 other

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RESULT 11
BALT2775/C
ID APP21725 Standard; cDNA; 1571
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                       당
                                                                                                                 AAC98907/c
                                                                                                                                                                                              Ouery Match
Best Local Similarity 89.5
Matches 17; Constructive
Cable Exp. Lat.
                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and reatment of the ansport, metabolic, neurological, reproductive, Cardiyascular --- disorders, and real proliferations.
                                                                              AAC98907,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1999;
10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAR-2001 (1irst entry)
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                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 155-156; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; transport disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human transport protein TPPT-25 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide with a human transport protein sequence is useful protein disorders associated with the immune, reproductive and cardiovascular systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lal P, YELL
Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2000; 2000Wa-US16668
                                                                                             AAC98907 standard; cDNA; 1945 BP
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                                                                                                                                                                                                                                                             Sequence 1571 Bp; 52.2 A; 265 C; 289 G; 495 T; 0 other:
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                                                                                                                                                                                                                                                                                    disorders such as carcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mmune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60105
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MR. Awimzai Y.
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990S-0148177.
990S-0149357.
990S-0162287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                    83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillman JL, Tang
Lu DAM, Au-Young
                                                                                                                                                                                                       0;
                                                                                                                                                                                                                   Score 15.8;
Pred. No. 9
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                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Sandman C, oung J, Patterson C;
                                                                                                                                                                                                                    96,
                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                      2;
                                                                                                                                                                                                                              Length 1571;
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cc gynaecological, cardiant and antiinflammatory activities, and can be used cological, cardiant and antiinflammatory activities, and can be used color for diagnosing a pathological condition or a susceptibility to one in a cc subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cances antigens can be used to exponent the treat or prevent pancreatic disorders, especially cancer.

Agonists and antagonists to the antigens can be used to design nucleic calci hybridisation probes that can proved in chromosome mapping, linkage and dispositic methods. The proteins can be used to design nucleic calci hybridisation probes that can proved in chromosome mapping, linkage and dispositic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including the proteins can be used to proteins can be used to protein can be used t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; prollferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENORE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC58773 to AAC59231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1: Page 594-595; 1379pp: English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a pancreatic cancer untigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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Matches 17
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                                                                                   1203 TITACTCCTGCCAGAGCTT 1185
                    AAY22956;
                                       AAV22956 standard; DNA;
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                                                                                                                             17; Conserv
                                                                                                                            Conservative
(first entry)
                                                                                                                                     83.2%
                                        5003 BP
                                                                                                                                0;
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Pred. No. 98;
0; Mismatches
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Sequence 1945 BP; 533 A; 3-0 C; 477 G;

552 T; 13 other;

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	1999	1999	1999	9	Ö	1999	Ö	9	1999	1000	1999	1999	1999	1999	1999	1998	1999	.1999	1999	·1999	1999	1999	-1999	1999	-1999	-1999	9995	$\boldsymbol{\vdash}$	$\vdash$	-1999	<u> </u>	י ל		9 6	J 1.	-1000	1000		1999	-1999	19		٠.	199		4 د	-	-1999	-1000	ر د	1000	12999			-	1.3	-	1-4		⊷.		-	4-3	-1999		100	555 L-	-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            defects, periodontal disease or healing of various types of tissues and wounds. They can also increase neuronal, astrocytic and gilal cell survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in neuronal survival and repair. They can also exhibit properties such as angiogenic, chemotactic and/or chemoattractant properties, and effects on cells including induction of collagen synthesis, fibrosis, differentiation responses, cell proliferative responses and responses involving cell adhesion, migration and extracellular matrices: These properties make the proteins potential agents for wound healing, reduction of fibrosis and reduction of scar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon of the genomic DNA for human bone morphogenetic protein-16 (BMP-16). Human BMF-16 is a homologue of a murine protein celled modal, which is expressed in the mouse node during gastrulation. The BMP-16 proteins can induce the formation of bone, cartilage or other connective tissue. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated bone morphogenetic protein-16 - used to develop products for inducing formation of bone, cartilage and other connective tissue, particularly for wound healing and tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of the second exon of human BMP-16
Ovis aries
                             Mammary gland factor; signal transduction; lactogenic hormone; cytokine regulated transcription factor; transgenic animal; sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be used for treating bone, cartilage or other connective tissue
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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA clone (AAT10554) coding for mammary gland factor (MGF) (AAR88199) was obtd. from a cDNA library derived from sheep lactating mammary tissue mRNA using probes (AAT10555-56) based on internal peptides of MGF. The cDNA is used to produce recombinant MGF in host cells, or as a probe. Transgenic animals, e.g. sheep, overexpressing MGF can be produced in order to increase milk producer to produce a therapeutically useful protein.
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Perfect score:
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2: /cgn2_6/ptodatc4/2.

3: /cgn2_6/ptodatc4/2.

4: /cgn2_6/ptodatc4/2.

5: /cgn2_6/ptodatc4/2.

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Score Pred. 0; Mis	O02 CUS CUS	ALIG	US-08-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
                                                                                                Sequence 3, Application US/08715202A Patent No. 5965403
                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                         Query Match
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                                                                              GENERAL INFORMATION:
                          APPLICANT: CELESTE, ANTHONY J.
APPLICANT: MURRAY, BETH L.
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-16 (BMP-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-POS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: GENETICS INSTITUTE,
STREET: 87 CAMBRIDGEPARK DRIVE
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CELESTE, ANTHONY J.
APPLICANT: MURRAY, BETH L.
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-16 (BMP-16)
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                            412 TCTGCTCCTGCGAGAGGTT 394
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LOCATION: 511..840
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DEDNESS: single
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COMPOSITIONS
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Pred. No. 20
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RESULT 4
US-08-366-276-1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,202A
FILING DATE: September 18, 1996
CLASSIFICATION: 514
ATTORNEY/AGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 498-8260
TELERAX: (617) 876-8851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERESTICS:
LENGTH: 2002 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08366276
Patent No. 5534409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
APPLICATION NUMBER: US/08/366,276 EILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9409396.0 EILING DATE: 11-MAY-1994 ATTORNEY_AGENT INFORMATION: NAME: Elmer, James Scoot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Groner, Bernd
APPLICANT: Goullleux, Fabrice
APPLICANT: Makao, Hiroshi
TITLE OF INVENTION: Cytokine Regulated Transcription Factor
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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NAME: LAZAR, STEVEN R
REGISTRATION NUMBER: 32,6
REFERENCE/DOCKET NUMBER:
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ZIP: 02140
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Pred. No. 23;
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us-08-373-579-5
PRIOR APPLICATION DATA:

PRIOR APPLICATION UNBER: US 08/319,932

PRIOR APPLICATION UNBER: US 08/319,932

PRIOR DATE: 07-0CT-1994

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 330-D

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 11.
SEQUENCE CHARACTERISTICS:
LENGTH: 2818 base pairs
TYPE: nucleic acid
CTENEREPERISES
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/348,492 FILING DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/373,579 FILING DATE: 17-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                 APPLICATION NUMBER: US 08/330, 261
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tarrytown New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08373579
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777 Old Saw Mill River Road
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244..2625
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                                                                                                                                                                                                                                                                                            US 08/353,503
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                               ; NAME/KEY:
; LOCATION:
US-08-373-579-5
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US-08-418-595-5
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GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserv
                                        TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 27-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 17-UAN-1995
FILING DATE: 17-UAN-1995
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STREET: ///
CITY: Tarrytown
CITY: New York
"STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
                                                                                                                                                                                   APPLICATION NUMBER: US 0: FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER OF SEQUENCES:
                                                                                                                                   NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: RE
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TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tttgctcctgccagaggt 18
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357.,1847
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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        Score 14.8; I
Mismatches
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                  1;
                  Length 2282;
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APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0. APPLICATION NUMBER: US/08/418,595 FILING DATE: 06-APR-1995 Application US/08418595 E: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill River Road et al. 4: TIE-2 LIGAND, METHOD OF MAKING AND USES 4: THEREOF US 08/319,932 US 08/330,261 Release #1.0, Version #1.30 us 08/373,579

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC TOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
                                                                                   Query Match
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Matches
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NFORMATION FOR SEQ ID NO: 5:
488 TTTCCTCCTGCCAGAGAT 505
                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                       NAME/KEY:
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                  1 tttgctcctgccagaggt 18
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                                                                     Local
                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                           NAME: Robert J. Cobe
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10591-6707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Tarrytown
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                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
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                                                         l Similarity
16; Conserv
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357..1847
                                                                                                                                                                                                                            2282 base pairs
                                                                                                                                                                                          unknown
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ENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
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88.9%;
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                                                                  Score 14.8;
Pred. No. 75;
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Pred. No. 75
                                                     Mismatches
                                                                               DB 2;
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US-09-162-437-5 RESULT

RESULT 9
US-08-447-411-44
: Sequence 44, Application US/08447411
: Patent No. 5773243

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                                                               Query Match
Best Local Similarity
Matches 16; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
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                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
488 TTTCCTCCTGCCAGAGAT 505
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (914) 345-7400
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APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-APR-1995 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
                                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cobert, Robert J. REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                       1 tttgctcctgccagaggt 18
                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US OFFILING DATE: 07-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                        1: 2282 base pairs nucleic acid
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                                                                     Conservative
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17-JAN-1995
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, 345-7721
, NO: 5:
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                                                                                   Score 14.8;
Pred. No. 7
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                                                                   Mismatches
                                                                                                   DB 4;
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                                                               Gaps
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CORRESPONDENCE ADDRESS:

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; LOCATION:
US-08-447-411-44
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPA: (703) 413-2220
TELEFAX: (703) 413-2220
TELEX: 24865-DATI UR
INFORMATION FOR SEC ID NO: 44:
SEQUENCE CHARACTERISTICS:
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Best Local S
                                                                                                                          Sequence 1, Application Patent No. 5922320
                                                                                                                                                                                                                                                                                                                Matches
                                                                                      GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08,
APPLICATION UNMBER: US 08,
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
                              APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
TITLE OF INVENTION: RECOMBINANT PROCVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, STATEM.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                        1 tttgctcctgccagaggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                            Application US/08662227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5924 base pairs
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BREDEHORST, REINHARD
VOGEL, CARL-WILHELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
70..4929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                          4..4929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA ENCODING COBRA C3, CVF1, AND CVF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1126-101-0
                                                                                                                                                                                                                                                                                                                                Score 14.8;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                 Length 5924;
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US-08-359-705B-7/c ; Sequence 7, Application US/08359705B ; Patent No. 5844092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE_DOCKET NUMBER: 1126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHAN: 703-413-3200
TELEPHAN: 703-413-220
TELEPHAN: 703-413-220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5948 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.9%;
Best Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/
FILING DATE: 08/10/94
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 20-Dec-1994
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Urfer, Roman
TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
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ADDRESSEE: P.C.
ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Fi
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Francisco
                                                                             08/286846
                                                                                                                                                                                                                                                     US/08/359,705E
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.44 Mb floppy disk
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Pred. No. 87
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RESULT 12
US-08-286-846A-7/c
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      Matches
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                    Best Local
                                  Query Match
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Best Local Similarity
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APPLICANT: Presta
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                                                                                                                                                                  TELEX: 910/371-7168

NFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shelton, David L. APPLICANT: Urfer, Roman
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIILE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 05-Aug-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    STRANDEDNESS:
                                                                                                                                    TYPE: Nucleic Acid
                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1858 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 tgctcctgccagaggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: TOICHIA, PhD., Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: P0873P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER ( 08/215139) FILING DATE: 03/18/94 ( )
                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                1858 base pairs
                                                                                                                                                                                                                      415/952-9881
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                                                                                                      SS: Single
Linear
                 75.8%;
93.8%;
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93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                    (Genentech)
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 Score 14.4; DB 2;
Pred. No. 1.2e+02;
0; Mismatches 1;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                 Length 1858;
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   Indels
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Gaps
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                                                                                                         Sequence 7, Application US/08444622A Patent No. 6025166
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                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DALL.

CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/444,622
APPLICATION NUMBER: US/08/286846
                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
APPLICANT: Leonard G. Presta
APPLICANY: David L. Shelton
APPLICANY: Roman Urfer
TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR
                                                                                                                                                                                                           545 TGCTCCTGCCAGAGCT 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Torchia, PhD., Tir
REGISTRATION NUMBER: 36.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94080
                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                       1858 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      David L.
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roman Urfer
                                                                                                                                                                                                                                                                                                                                                                            Linear
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David L. Shelton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                         Single
                                                                                                                                                                                                                                                                                           75,8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/457,880A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Timothy E.
                                                                                                                                                                                                                                                                                         Score 14.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P0873P1C3
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                            4; DB 2;
1.2e+02;
                                                                                                                                                                                                                                                                                                            Length 1858;
                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                             0
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Genentech, Inc.

CITY: South San Francisco

California 1 DNA Way

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RESULT 15
US-08-942-562-7/c
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REGISTRATION NUMBER: 36,700
REFERENCE, DOCKET NUMBER: 90873P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPHONE: 650/25-981
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1858 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08942562
Patent No. 6027927
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Best Local Similarity 93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICATION NUMBER: US/08/942,562
FILLING DATE: 01-007-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/444,597
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Neteron Control 
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/444,622A
FILING DATE: 19-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech,
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Pred. No. 1.2e+02;
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FILING DATE: 19-May-1995

ATTORNEY/AGENT INFORMATION:
NAME: TOTCChia, PhD., Timothy E.
REGISTRATION UNMER: 36,700

REFERENCE/DOCKET NUMBER: P0873P1C2

TELEPHONE: 415/225-8674

TELEPHONE: 415/225-8674

TELEPAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION OR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
US-08-942-562-7
                  LENGTH: 1858 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear
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Query Match 75.8%; Best Local Similarity 93.8%; Matches 15; Conservative Score 14.4; DB 3; Length 1858; Pred. No. 1.2e+02; 0; Mismatches 1; Indels 0 0

Search completed: July 25, 2001, 05:18:55 Job time: 9218 sec

545 TGCTCCTGCCAGAGCT 530

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb\_est65:

est64: est63 gb\_est59

\_est57 est56 est54 egt52

est53

\_est61:

gb\_est81: gb\_est80:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

168: 169: 170: 171: 172: 173: 174: 175: 1775: 1776: 1777: 1779: 17

gb\_est97:\*
gb\_est98:\*
em\_esthum30:\*
em\_esthum31:\*
em\_esthum31:\*
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em\_estcon1:\*
em\_estco11:\*
em\_estro21:\*

gb\_est95:\*

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gb\_est107:\* gb\_est108:\* gb\_est109:\*

em\_estro23:\* em\_htc:\*

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	Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston R., Williamson, A., Wohldmann, P. and Wilson, R.  TITLE The WashU-Merck EST Project  JOURNAL Unpublished (1995)  COMMENT Contact: Wilson RK  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  Tel: 314 286 1800	ACCESSION R31201  VERSION R31201.1 GI:787044  KEYWORDS EST.  SOURCE human. ORGANISM Homo Sapiens Cutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo.  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 348) AUTHORS Hillier, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hutman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,	Qy lastgaactcoctcoctacctt 21	ORIGIN  Query Match  84.8%; Score 17.8; DB 188; Length 212;  Best Local Similarity 90.5%; Pred. No. 1.4e+02;  Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	/dev_stage"placenta obtained at birth (full term)" /lab_host="DH10B (ampicillin resistant)" /note="Organ: placenta; Vector: pT773D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer {5' AACTGGAAGAATTCCGGCCGCAGGAATTTTTTTTTTTTT	Source: IMAGE Consortium, LLNL  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 761 Std Error: 0.00  Seq primer: M13RP1  High quality sequence stop: 74.  FEATURES  Location/Qualifiers  1. 212  /organism="Homo sapiens" /db_xref="GDB:44134" /db_xref="Taxon:9606" /clone="IMAGE:137806" /clone="IMAGE:137806"	TITLE The WashU-Merck EST Project JOURNAL Unpublished (1995) COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 761 High quality sequence stops: 74

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FEATURES

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Query Match
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                    Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Insert Length: 774 Std Error: 0.00
                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                             .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldman,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

Hillier; L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Size: 774
High quality sequence stops: 306
                                                                                                                                                                                                                               Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R67982 417 bp mRNA EST OI-JUN Y104a10.rl Soares placenta Nb2HP Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
   Seq primer: M13RP1
                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                             R67982.1 GI:841499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMAGE Consortium (info@image.llnl.gov) for further information insert Length: 728 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGE:138234 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares placenta Nb2HP"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:134282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism-"Homo sapiens"
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90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.8; DB 18
Pred. No. 1.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     では、「一個の場合をある」というできませる。
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 348;
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ORIGIN
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KEYWORDS
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R31714
LOCUS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                        source
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                                                                                                                       High quality sequence stop: 244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 a
                                 /organism="Homo sapiens"
/db_xref="GDB:540219"
/db_xref="taxon:9606"
/clone_lib="Soares placenta Nb2HP"
                    /clone="IMAGE:134398"
                                                                                                     ocation/Qualifiers
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High quality sequence stop: 306.
 Conservative
                                                                          constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                           /clone_lib="Soares placenta Nb2HP"
                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:138234"
                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:544609"
         90.5%;
                                                                                                                                                                                                                                                     on/Qualifiers
 0;
Score 17.8; DB 18
Pred. No. 1.6e+02;
0; Mismatches 2
                    DB 188;
                     Length 417;
  0;
  Gaps
  0;
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.M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project Email: est@watson.wustl.edu Insert Size: 707 High quality sequence stops: 244 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 R31714 418 bp mRNA EST 28-APR-yh63a12.rl Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:134398 5', mRNA sequence. Unpublished (1995 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. R31714.1 GI:787557 (bases 1 to 418) 28-APR-1995

SOURCE ORGANISM

REFERENCE

AUTHORS

COMMENT

JOURNAL

TITLE

RESULT R67982

DEFINITION

ACCESSION KEYWORDS ERSION

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Matches

BASE COUNT

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                       Seq primer: M13RP1
                                                                                                                                                                                                                                                                                    Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoeimage.llnl.gov) for further information.
Insert Length: 769 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 769
High qality sequence stops: 411
                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 bp mrnA
yiOlall.rl Soares placenta Nb2HP Homo
IMAGE:137948 5', mrnA sequence.
R63154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 481)
Hillier, L., Clark, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Me.azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                 clone_lib-"Soares placenta Nb2HP"
                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:137948"
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:544291"
                                                                                                                        'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.8;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens cDNA clone
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Query Match
Best Local S
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SOURCE ORGANISM

VERSION ACCESSION

KEYWORDS

REFERENCE

AUTHORS

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DEFINITION LOCUS B

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BASE COUNT ORIGIN

COMMENT

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FEATURES

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19

Conservative

Similarity

84.8%; Score 17.8; DB 235; Length 498; 90.5%; Pred. No. 1.6e+02; tive 0; Nismatches 2; Indels 0;

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BASE COUNT
ORIGIN
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AUTHORS
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ORGANISM
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AQ882343
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 aagtgaactccctgctacctt 21
                                                                                                                                                                                                                                                                                               High quality sequence stop: 498.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  http://www.htsc.washington.edu
Plate: 9150 row: C column: 5
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 498)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ882343 498 bp DNA GSS 09-NOV-1999
HS_5382_Al_B03_T7C RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=9150 Col-5 Row-C, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11, For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ882343
                        155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
              Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EccRI and EcoRI Methylase. Size selected DNA was cloned into the DBAC63.6 vector at EccRI sites"

111 c 118 g 111 t 3 others
                                                                                                                                                                             /db_xref="taxon:9606"
/clone="plate=9150 Co1=5 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                   1. .498
                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                      'organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:6313810
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90.5%;
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Pred. No. 1.
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2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holzman, T.,
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AQ185931/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 608) Theorem (bases I to 608) Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                       AQ551067 608 bp DNA GSS עפרים RPCI-11-416M22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-416M22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ185931 510 bp DNA GSS U1-NOV-1998 HS_3065_Al_D09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Place-3065 Col-17 Row-G, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 510)
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                                                                                                                                                            , DNA sequence.
AQ551067
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Location/Qualifiers
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E-Coli DH10B"
98 c 100 g 153 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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Pred. No. 1
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AV553454/c
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter de jong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV553454 471 bp mRNA EST 07-SEP-2000 AV553454 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.C. Y.C. End Sequences from Library RPCI-II for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clone RZ63b05R 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hbe@tigr.org
                                                                                                                                                The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                          Contact: Erika Asamizu
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                                                                                                        1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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152 c 134 g 143 t
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/clone="RPCI-11-416M22"
/clone_11b="RPCI-11"
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/cell_type-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                      /organism="Arabidopsis thaliana"
/strain="Columbia"
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/db_xref="taxon:3702"
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0; Mismatche
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Best Local Similarity
Matches 18; Conserv
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hes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-QV0&t2-QV0-HT0310-
061299-069-g93&t3-1939-12-06&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 17
High quality sequence stop: 193
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                       Conservative
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                                                                                                                                                                                                /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0310"
                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
xhor"
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/clone_lib="Arabidopsis thaliana roots Columbia"
/tlssue_type="roots"
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100.0%; Pr
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Pred. No. 4.4e+02;
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Pred. No.
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4.1e+02;
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                                                                                                   Indels
                                                                                                                                   Length 193;
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source
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Contact: Marra M./Nouse EST Project
Washin-HHMI Nouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 295.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Woore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA500281 304 by
vi97f08.rl Barstead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:532415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 304)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
          74 a
/db_xref-"taxon:10090"
/clone-"IMAGE:920199"
                                                                                                                                                                                                                                              /tissue_type="pooled organs"
/dev_stage="7 day"
                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                        /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                 /clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                             /strain-"FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism-"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis, MO 63108
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Query Match
Best Local Similarity 152 AAGTGAACTCCCTGGTTCCT 171 1 magtgaactccctgctacct 20 vl20g01.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:972816 5', mRNA sequence.
AA560193
AA550193.1 G1:2331558 Conservative 90.0%; 0 Score 16.8; DB 8; Pred. No. 4.8e+02; 0; Mismatches 2; Length 304; Indels 0;

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10-03-122-030-3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aagtgaactccctgctacct 20
                Contact: Marra M/Mouse EST Project
                                      Waterston, R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                     AA620205 410 bp mrNA EST VO64806.rl Soares_mammary_gland_NbMMG Mus m IMAGE:1054642 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
WashU-HHMI Mouse EST Project
                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 410)
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mürinae; Mus
                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                         AA620205.1 GI:2524081
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Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Woore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                     house mouse.
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WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Stratagene mouse Tcell 937311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:972816"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 9;
Pred. No. 4.8e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                           musculus cDNA clone
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                                                                                                                                              Dietrich, N., Dubuque, T.,
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI615361 416 bp mkNA
v197f08.y1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA
clone IMAGE:920199 5' similar to TR:075935 075935 DYNACTIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                   Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                        Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                 AI615361.1 GI:4624528
EST.
                                                                                                                                                                                                                                                                                                                                                                                             house mouse
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia). digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary gland; Vector: p7773D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="mammary gland"
/dev_stage="4 weeks"
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/clone="IMAGE:1054642"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NbMMG"
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/strain="C57BL/6J"
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                                                                                     Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AAGTGAACTCCCTGGTGCCT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 aagtgaactccctgctacct 20
                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                   Seq
                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:580978
                                                                                                                                                                                                                                                                                                    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                        Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 439)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA616429 439 bp mRNA EST 07-OCT-1997 vo09e02.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1049402 5', mRNA sequence.
                                                                                                                                                                                                                                                                                     Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA616429.1 GI:2503634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -40RP from Gibco
High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector to vector length is 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               correct orientation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:532415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) for further information.
                primer: -28m13 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="TMAGE:920199"
/clone_lib="Barstead mouse pooled organs MPLRB4"
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/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.8; DB 22; Pred. No. 5e+02; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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BASE COUNT
                                                 ORIGIN
Query Match 80.

Best Local Similarity 90.

Matches 18; Conservative
                                                                                                                                                                                                                                              source
                                                          105 a
                                                     /strain="C3H"
/db_xref="taxon:10090"
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        80.0%;
Score 16.8; DB 9;
Pred. No. 5.1e+02;
0; Mismatches 2;
                  Length 439;
0
Gaps
0
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В Ş 214 AAGTGAACTCCCTGGTGCCT 233 1 magtgaactccctgctacct 20

Search completed: July 25, 2001, 04:54:49 Job time: 10422 sec

Run

05:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg length: 0 seg length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
                             999.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 July 25, 2001, 05:18:51; Search time 117.39 Seconds (without alignments) 33.141 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317530 segs, 92630169 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-142-095-2
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccactgggatcaacagtatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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                      PCT-US92-00282-18
PCT-US92-00282-1
US-08-960-780-37
US-08-960-780-37
US-08-454-028-3
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US-08-96-36-17
US-08-96-36-17
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                   Sequence 18, Appl Sequence 37, Appl Sequence 37, Appl Sequence 17, Appl Sequence 37, Appl Sequence 38, Appl Sequence 39, Appl Sequence 36,                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
US TO DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
PCT-US92-00282-18/c
Sequence 18, Application PC/TUS9200282;
GENERAL INFORMATION:
                                                                                                                                                            ; STRANDEDNESS: si;
; TOPOLOGY: linear
; MOLECULE TYPE: cDN:
PCT-US92-00282-18
                                                                                Query Match
Best Local Sim
Matches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 0
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                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282 FILING DATE: 1992010
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, NAPISON T.
REGISTRATION NUMBER: 26581
REGISTRATION NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
TELEPAX: 202-822-0944
                                                                                                                                                                                                                                   TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OWENS, 1DA 5.
APPLICANT: RITTER, JOSEPH K.
APPLICANT: RITTER F. JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 190 CCACTGGGATCAACAGTATCT 170
                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20036-5601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                          ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: CUSHMAN DARBY & CUSHMAN 1615 L STREET, N.W.
                                                                                100.0%;
ilarity 100.0%;
Conservative 0;
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US-08-906-480-13
US-08-906-480-17
US-08-906-480-16
US-08-906-480-16
US-08-589-939-4
US-08-589-735-1
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US-09-026-985-58
US-09-026-985-58
US-08-387-117-7
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                                                                                              Score 21; DB 5;
Pred. No. 0.075;
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Version

#1:25

Result

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Minimum

ALIGNMENTS

Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 16, Appli Sequence 14, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 54, Appli Sequence 58, Appli Sequence 59, App

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Mismatches

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Length 1190;

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PCT-US92-00282-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2336 been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, KATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9153
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Flor-
COMPUTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·US92-00282-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
                                   APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cobn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                                                                                              ERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       106 CCACTGGGATCAACAGTATCT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: THE GENE
                                                                                                                                                                                                                                                                                                                                                                                                           1 ccactgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELEPHONE: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: POFILING DATE: 19920110
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                                                                                                                                                                                                                                                                                            Application US/08960780
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 5; ilarity 100.0%; Pred. No. 0.082; Conservative 0; Mismatches
                                                                                                                                                              Stockhoff, Brian A. Schmeits, James
                                                                                                                                                                                                   Narva, Kenneth E.
                                                                                                                                                                                                                 Schnepf,
                                                                                                                                                                                                                     Feitelson, Jerald S. Schnepf, H. Ernest
Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/09073898 Patent No. 6242669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic original source: INDIVIDUAL ISOLATE: 196F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1073 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 352-375-8100
                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 ACTGGGAAAAACAGTATCT 856
                                                                                                                                                              ITLE OF INVENTION:
ITLE OF INVENTION:
UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                         COUNTRY: US
ZIP: 32606-6669
                                                                       STATE:
                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                        CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: · linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 32606-6669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 actgggatcaacagtatct 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                       EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                       E: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1073 base pairs
                                                                                                                                                                                        Finstad-Lee, Stacey
VENTION: No. 6242669e1
                                                                                                                                                                                                                                                              Dullum, Charles Joseph
Muller-Cohn, Judy
                                                                                                                                                                                                                                                                                                                    Stockhoff, Brian A. Schmeits, James
                                                                                                                                                                                                                                                                                                                                                                     Feitelson, Jerald S. Schnepf, H. Ernest
                                                                                                                                                                                                                                                 Stamp, Lisa
                                                                                                                                                                                                                                                                                                  Loewer, David
                                                                                                                                                                                                                                                                                                                                                      Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.2%;
89.5%;
                                                                                                                                                                             No. 6242669el Pesticidal Toxins and Nucleotide Sequences Which Encode These Toxins
                                                                                                                                                                                                                                  George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/960,780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA-708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8;
Pred. No. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1073;
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: INDIVIDUAL ISOLATE: 196F3
US-09-073-898-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-403-853-17
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5844094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                            CURRENT APPLICATION DATA: 9/08/403,853
APPLICATION NUMBER: US/08/403,853
PILING DATE: 30-AMY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/960,780 FILING DATE: 30-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                          PPLICANT: COLMAN, Peter M. INDING POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        838 ACTGGGAAAAACAGTATCT 856
                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                        STREET:
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REFERENCE/DOCKET NUMBER: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sanders, Jay M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/073,898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                    20007-5109
                                                                                                                                                                                                                                                    Washington
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                                                                                                                                                                                                                                                                                                                                                                       KORT, Alex A.
KORT, Alex A.
IRVING, Robert A.
ATWELL, John L.
MALBY, Robyn L.
POWER, Barbara E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08403853
                                                                                                                                                                                                                                                                    3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352-372-5800
                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUDSON, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                         Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352-375-8100
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89.5%;
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Pred. No. 29;
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US-08-403-853-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08473496 Patent No. 5700660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,496
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277,492
FILING DATE: 19-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Jack L. Leonard
APPLICANT: Peter E. Newburger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEC 1D NO:
                                                                         PRIOR APPLICATION DATA: 08/06
APPLICATION NUMBER: 08/06
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 50% or 55%
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO POFILING DATE: 24-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          575 ACTGGTATCAACAGAATC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELLEFAX: (-
TELEFAX: 904136
                  NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/078001
                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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1..819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITIONAL CONTROL OF SELENIUM INSERTION IN POLYPEPTIDES FOR X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.5%;
88.9%;
                                                                                                                08/066,680
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Pred. No. 88;
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Length 831; Indels

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Matches

16; Conservative ... 0;

Mismatches

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US-08-454-028-3
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                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/Z Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: MOTEDETECT (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION MISSER: US/08/454,028

FILING DATE: May 30, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/06
FILING DATE: May 24, 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jack L. Leonard
APPLICANT: Peter E. Newburger
TITLE OF INVENTION: POST-TRANSCRIPTIONAL GENE REGULATION BY
TITLE OF INVENTION: SELENIUM
                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                             TOPOLOGY:
                                           STRANDEDNESS:
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                            ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                     832 base pairs
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                                                                                                                                          (617) 542-8906
                        linear
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ON: 435
                                         single
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Pred. No. 88;
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Best Local Similarity

70.5%; 88.9%;

Score 14.8; DB 2; Pred. No. 88;

Length 832;

Query Match

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PCT-US95-09121-1/c
                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                      PCT-US94-05388-3
                                                                                                             Sequence 1, Application PC/TUS9509121 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application PC/TUS9405388 GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             768 ACTGGGATCAACAGGACC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 04.
REFERENCE/DOCKET NUMBER: 04.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617): 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/066,680 FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jack L. Leuna...
APPLICANT: Peter E. Newburger
APPLICANT: POST-TRANSCRIPTIONAL GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                            70.5%;
Local Similarity 88.9%;
les 16; Conservation
                                                                                                                                                                                                                   3 actgggatcaacagtatc 20
                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 16 May 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              768 ACTGGGATCAACAGGACC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fish & Richardson
                                          X-RAY CRYSTALLOGRAPHY
                                                     POSITIONAL CONTROL OF SELENIUM INSERTION IN POLYPEPTIDES FOR
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RESULT 10
PCT-US96-07496-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
              APPLICATION NUMBER: PCT/US96/07496 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 MODEL 50Z OF 55ZX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDFORFECT (Version 5.1)
CURRINT APPLICATION DATA:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                     APPLICANT: University of massachusetts medical Center TITLE OF INVENTION: POST-TRANSCRIPTIONAL GENE REGULATION BY TITLE OF INVENTION: SELENIUM
                                                                                                                                                                                                                                                                    UMBER OF SEQUENCES:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     768 ACTGGGATCAACAGGACC 751
                                                                                                                                               COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,496
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSICATION:
CLASSICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 08/277,492
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or
                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04020/078W01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/09121
FILING DATE: 19 July 1995
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FILING DATE: 19 July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                      Boston
                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                     Application PC/TUS9607496
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Pred. No. 8
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US-08-698-551-13/c
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 TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIOWN, SCOtt A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
TELEPHONE: %(617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08698551 Patent No. 5712381
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Matches 16;
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REFERENCE/DOCKET NUMBER: 0402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Graham, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/066,680
APPLICATION NUMBER: 1993
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APPLICATION NUMBER: 08/454,028
FILING DATE: May 30, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
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Pred. No. 88;
0; Mismatches
行在 法 人名 語語 正教 持續人 係 公子
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; LOCATION: US-08-602-228-13
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US-08-698-551-13
         Matches 16;
                                     Query Match
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Patent No. 5843675
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local :
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NFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3225 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
APPLICANT: Schievella, Andrea
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING
NUMBER OF SEQUENCES: 16
                                                                                                                                                         OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: DC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                         YPOTHETICAL:
                    Local Similarity
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ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CI
                                                                                          NAME/KEY: CDS
LOCATION: 3..2846
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                STRANDEDNESS: double
                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
STATE: Massachus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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16; Conservative
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       Conservative
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               70.5%;
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 Score 14.8; DB 2; Length 3225;
Pred. No. 1e+02;
0; Mismatches 2; Indels 0
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Pred. No. 16
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RESULT 14
US-08-839-032A-13/c
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                                                                                                        Sequence 13, Application US/08839032A
Patent No. 5891675
                                                                                                                                                                                                                                                                        Matches
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                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR EGO ID NO: 13
SEQUENCE CHARACTERISTICS:
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND PROTEINS
                                 APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A,
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
APPLICANT: Graham, James
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LOCATION: 3..2846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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; Sequence 13, Application US/08839031A
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                                                                                                                                                                                                                                                      PATENT NO. 5946638
GENERAL IMFORMATION:
APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL THE RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
CORPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTMARE: Patentin Release #1.0, Version #1.25

CURRENT'APPLICATION DATA:

APPLICATION NUMBER: US/08/839,031A
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3225 base pairs
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NAME: BIOWN, SCOLT A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GISTELECOMMUNICATION INFORMATION:
TELECHNOE: (617) 498-8224
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/839,032A
FILING DATE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
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                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                          STREET: 87 CambridgePark Drive CITY: Cambridge
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LOCATION: 3...
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STRANDEDNESS: double
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NAME/KEY: CDS
LOCATION: 3..2846
US-08-839-031A-13
Search completed: July 25, 2001, 05:18:52 Job time: 9215 sec
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NAME: Springer, Suzanne A.,
REGISTRATION NUMBER: 41,323
REFERENCE/DOCKET NUMBER: 615232BDIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                             Ouery Match 70.5%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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LENGTH: 3225 base pairs
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CLASSIFICATION:
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Pred. No. 1e+02;
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Gaps

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Listing first 45 summaries
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gb\_est59:

gb\_est79 gb\_est76

gb\_est82 gb\_est81

b\_est85:

b\_est84

gb\_est65:

gb\_est64 gb\_est63 gb\_est61: gb\_est60

gb\_est75

gb\_est62:

gb\_est53:\*
gb\_est55:\*
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gb\_est52:

gb\_est48:\*
gb\_est50:\*
gb\_est51:\*

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9b_gs33: *
9b_gs33: *
9b_gs34: *
em_gss_rod6: *
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em_gss_hum4:*
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gb\_est105: gb\_est106: gb\_est67:\* gb\_est68:\*

gb\_est102

gb\_est90

b\_est88

gb\_est73:\*
gb\_est74:\*
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gb\_est97:\*
gb\_est107:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AUTHORS
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 327)

Hillar, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Districh, N., DuBuque, T., Favello, A., Gish, W., Hawkins
,M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore
,M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
                                                                                                                                                           yc50a04.rl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:84078 5' similar to gb:M57899 UDP-GLUCURONOSYLTRANSFERASE 1A
                                                                                               Homo sapiens
                                                                                                                                                 PRECURSOR, MICROSOMAL (HUMAN);, mRNA sequence.
                                                                                                                                T71061.1 GI:685582
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AU070697 AU094227

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BF598564 sv19a09.y

BG557402 EM1_43_E0

AQ77479 HS_3195_A

BF193631 245281 MA

AZ911013 RPCI-24-1

BF194355 246337 MA

AZ92004 TM0310P03
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AG013064 Homo sapi
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                  1 ccactgggatcaacagtatct 21
                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 383)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucabb,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Washi-Merck EST project 1997
                                                                                                                                                                                                                  AA195421
AA195421.1
                    Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                          AA195421 383 bp mRNI
zr36h09.sl Soares_NhHMPu_S1
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                  similar to
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Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, Funderwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 290.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Stratagene liver (#937224)"
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/clone="IMAGE:84078"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                  contains element MSR1
                                                                                                                                                                                                                  GI:1785114
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Pred. No.
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2.2;
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mes 19; Conserv
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large
                                                                                   Genoscope
                                                                  Direct Submission
                                                                                                                                                                                           Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                        Tetraodon nigroviridis DNA
                                                                                                                                                                                Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                       Bouneau, L., Billault, A., Quetier, F., Saurin, W., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis. Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 099M21 of library G from Tetraodon nigroviridis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                               Roest-Crollius, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS; genome survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                     (bases 1 to 1078)
                                                                                                                                                                                                                                                      (bases 1 to 1078)
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                                                                                                                                                                gene number estimate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-Torgan: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHFU, and fetal heart NbH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479 " 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rt Length: 1881 Std Error: 0.00 quality sequence stop: 218.
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/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
/db_xref-"GDB:5427569"
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                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2&t2=IL2-CS0048-301000-198-G10&t3-2000-10-30&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baía, G.S., Simpson, D.H., Brunstein, A., deOliveita, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
1 (bases 1 to 297)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE764030 297 bp mRNA EST 12-JAN-2001 ILZ-CS0048-301000-198-G10 CS0048 Homo saplens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF764030.1 GI:12111930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/note-"Organ: colon_est; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                         /dev_stage="Adult"
                                                                                                                                                                             /db_xref="taxon:960
/clone_lib="CS0048"
                                                                                                                                                                                                              /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                 ty sequence stop: 58.
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/note="Genoscope sequence ID : C0BG099AG11Sp1-end :
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/db_xref="taxon:99883"
/clone="099M21"
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Pred. No. 59;
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Shatsman, S.,

Akinret

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AUTHORS
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    AND COME SECTION OF SECTION I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1873 Std Error: 0.00
                                                                                              Similarity 90.5%; Pred, No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Laey, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washd-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA195418 425 bp mRNA EST 06-AUG-1997 zr36g10.sl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665538 3/similar to contains element MER5 repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                    Conservative
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Location/Qualifiers
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                                                                                                                                                                                                 Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.
                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Pooled human melanocyte, fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB;5427570"
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Pred. No. 96;
                                                                               Mismatches
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                         AU030401 499 bp mRNA EST 19-OCT-1998 AU030401 Rice CDNA from immature leaf incliding apical meristem Crysa sativa CDNA clone E51014_42, mRNA sequence.
                                                                                                                                                                                                                                                                               19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/Orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

plate: 392 row: B column: 4
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, S., Nierman, W., Feldblyum, T., Malek, J.,
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1 (bases 1 to 612)
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C575L/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the
                                                                                                                                                                                                                                                                                                                                                                                             ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). * 121 c 116 g 199 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="RPCI-23-392B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain-"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex-"Female"
                                                                                                                                                                                                                                                                                              84:8%;
90.5%;
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                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                  Score 17.8; DB 237;
Pred. No. 1.1e+02;
O: Mismatches 2;
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Length 612;

0; Gaps

0:

Andrews State Stat

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FEATURES
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BF700745
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                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
               Plate: LLCM1120 row: c column: 11 High quality sequence stop: 623.
                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BF700745
                                                                                                                                                                                                                                                                                                                                                                                                                             BF700745 624 bp mRNA EST 22-DEC-2000 62128542F1 NIH_MGC_56 Homo saptens CDNA clone IMAGE:4285378 5',
                                                     found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
                                                                              CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 624)
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takuji Sasaki
mational Institute of Agrobiological Resources
Rice Genome Research program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROJECT -'RGP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 0298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice cDNA from immature leaf including apical merister
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 499)
Sasaki, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 0298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU030401.1 GI:3763649
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E51014_42"
/clone_lib="Rice cDNA from immature leaf including apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="immature"
/note="organ: leaf; immature leaf including apical
meristem (under long day condition)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Oryza sativa"
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 g
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JOURNAL
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                                                                                                                                                                                                                                                                                              High quality sequence stop: 399.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amegsham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    z197g08.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA AA7R97a
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 437)
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/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGGGCGAGTG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Paio Alto, CA)."
/dev_stage="20 week-post conception fetus"
/lab_host="0B10B (ampicillin resistant)"
/note="organ: Liver and Spieen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                          /clone_lib="Soares_fetal_liver_spleen_lnFLS_S1"
/sex="male"
                                                                                                                                                                                                /db_xref="GDB:1353023"
/db_xref="taxon:9606"
                                                                                                                                                                              /clone="IMAGE:448766"
                                                                                                                                                                                                                                                organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:2836953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.0%; Score 17;
100.0%; Pred. No.
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2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            St. Louis, MO 63108
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enhartoideae; oryzae, Oryzae.

1 (bases 1 to 450)
Sasaki, T. and Yamanoto, K.
Rice DNA from panicle at flowering stage (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib-"Rice panicle at flowering stage"
/dev_stage-"flowering stage"
/note-"organ: panicle; Rice cDNA from panicle at flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF588564 484 bp mRNA EST 12-DEC-2000 sv19809.1d Gm-c1057 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1057.17 5' similar to SW:PLAS_LYCES P17340 PLASTOCYANIN PRECURSOR. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 484)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Hylie, T., Underwood, K., Sceptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swalter, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R., and Wilson, R., Jackson, Y., Cardenas, M., McCann, Public, Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 107;
Pred. No. 3.4e+02;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .450
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                          Tel: 0298-38-7441
Fax: 0298-38-7468
Emall: tsasaki@abr.affrc.go.jp
PROJECT - RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Nipponbare"
/db_xref="taxon:4530"
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                                                 AU094227.1 GI:8856909
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                   mRNA sequence.
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Enrhartoldeae, Oryzeae, Oryza
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Yamamotu, K and Sasaki, T.
Rice CDNA irom young root
Unpublished (1999)
Contact: Takuli Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Rice cDNA from young root"
/tissue_type="young root"
88 c 94 q 132 t
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0; Mismatches 2;
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Fax: 0298-38-7468
Email: tssaskieabr.affrc.go.jp
PROJECT - 'RGP'
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/db_xref="taxon:4530"
/clone="R10115_1A"
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                                                                                                                    The University of Georgia Plant Sciences Building, Fax: 706 542 1860
                               Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                   An EST database from Sorghum: developing embryos Unpublished (2000)
Seq primer: JEN REV
                                                                                            Email: mmpratt@uga.edu
                                                                                                                                                                                                                        Department of Botany
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sorghum.
Sorghum bicolor
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                  Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 520)
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                                                                                                                                                                                                                                                Cordonnier-Pratt MM
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/clone_lib="Gm-c1057"
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                                                                                                                                                                                                High quality sequence stop: 534
Location/Qualifiers
                                                                                                                                                                                                                                                                                  Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3195 row: C column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebruta; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominikke; Homo.

1 (bases 1 to 534)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzeli,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. at millioners.
                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618 Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ737479 534 bp DNA GSS 16-JUL-1999 HS_3195_AZ_B0Z_T7C CIT Approved Human Genomic Sperm Library D Homo Sapiens genomic clone Plate=3195 Col-4 Row-C, DNA sequence.
                                                                                                                                                                                                                                         Class: BAC ends
                                                                                                                                                                                                                                                             Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.
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                                                                                                                                                                                                                                                                                                                                               jwallace@u.washington.edu
                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones
E-Coli DH10B"
                                                                                    /db_xref="taxon:9606"
/clone_"plate=3195 Col=4 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                           /sex="male"
                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:4558"
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Best Local Similarity

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Score 16.8; DB 232; Length 534; Pred. No. 3.5e+02;

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Search completed: July 25, 2001, 04:54:51 Job time: 10424 sec
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FORWARD: AGGALAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 74 row: K column: 12
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
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1 (bases 1 to 535)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
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245281 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
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/db_xref="taxon:9823"
/clone_lib="MaRc 2PIG"
/tlssue_type="pooled"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: xbal; Site_2: xhol; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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A65502 Sequence 3 AF352795 Homo sapi AF180372 Homo sapi A55504 Sequence 5 D87674 Homo sapien AC006985 Homo sapi AC026497 Homo sapi AF297093 Homo sapi	Description

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Patent: WO 9732042-A 3 04-SEP-1997;
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/db_xref="taxon:32644"
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G31676 SWSS1282 Er
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Z84468 Human DNA
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MCKIe,K., Kutlar,F., Glendenning,M. and Kutlar,A.

7(TA) repeat polymorphism of the TATA box of human bilirubin

UDP-glucuronosyltransferase 1-1(UGTIAI*1) gene in a patient with

sickle cell anemia + high bilirubinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF352795 531 bp DNA PRI 10-APR-2001
Homo sapiens bilirubin UDP-glucronosyltrasferase 1-1 (UGT1A1) gene,
AF352795

    (bases 1 to 531)
    McKie, K., Kutlar, F., Glendenning, M. and Kutlar, A.

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Mammalla<sup>st</sup> Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/product="bilirubin UDP-glucronosyltrasferase 1-1"
/protein_id="AAK31204.1"
/db_xref="q1:13569709"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="repeat polymorphism compared to UGT1A1 sequence presented in GenBank Accession Number AF180372; contains 7 ta repeats frequently detected in patients with high bilirubinemia"
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/note="UGT1"
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/db_xref="taxon:9606"
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Kutlar, F., Sromek, E., Leithner, C., Nechtman, J. and Kutlar, A. Detection of the TATA box polymorphism of the human bilirubin UDP-glucuronosyltransferase 1-1 gene (UGT1*1) in a patient with sickle cell anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-AUG-1999) Medicine, Hematology/Oncology-Sickle Cell Center, Medical College of Georgia, 15th Street, AC-1000, Augusta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                              123
                                                                                                                                                                                         /protein_id="AAF01205.1"
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/translation="MAVESGGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSML
GAIQOLQQRGHEITVLAFDASIXIRDG"
124 c 141 g 153 t
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/replace="t"
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/protein_id="AAF01205.1"
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/tissue_type="whole blood"
.>541
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                      note="Ritter,J.K.,
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                                                                                                                                                                                         Submitted (04-SEP-1996) to the DDBJ/EMBL/GenBank databases. Hisao Ueyama, Shiga University of Medical Science, Department of Medical Biochemistry; Seta, Otsu, Shiga 520-21, Japan (Tel:077-548-2162, Fax:077-548-2164)
Sequence updated (08-Jan-1997) by: Hisao Ueyama.
Location/Qualifiers
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bilirubin UDP-glucuronosyltransferase
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Sequence 5 from Patent W09732042.
A65504
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                                                                                                                                                                                                                                                                                                                                                                                                      1 (sites)
Ueyama,H., Koiwai,O., Soeda,Y., Sato,H., Satoh,Y., Ohkubo,I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Patent: WO 9732042-A 5 04-SEP-1997;
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/note="XRE"
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                                                                                                                          /organism="Homo sapiens"
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/chromosome="2q37"
note-"HNF-1
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                                           Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Aug 13, 1999 this sequence version replaced g1:4337256.
                                                                                                                                  Submitted (22-OCT-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, 6 (bases I to 68770)
                                                                                                                                                                                                                                                    Submitted (13-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                   Submitted (05-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                           Direct
                                                                                                                         Waterston, R
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                 MO 63108,
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Homo sapiens BAC clone RP11-154L24 from
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Center: Washington University Genome Sequencing Center Center code: WUGSC
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
-------Summary Statistics
Center project name: H_NH0154L24
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An Improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-332L11, 200 bp overlap. Actual start of this clone is at base position 86134 of RP11-332L11; actual end is at base position 68770 of RP11-154L24.

The clone RP11-154L24 contains a tandem repeat from base positions 38234 to 39039, this region contains some low quality data. The assembly is consistent with the restriction digest information. FEATURES Location/Qualifiers source 1. .68770 /organism="Homo sapiens"

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Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Mcheeters, R.,
McIdrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Poy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J.,
Nicert Subries of Subries 
                                                                                                                                                                                                                                                                                                                              Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalla; Eutherla; Primates; Catarrhini; Honi

(bases 1 to 176619)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-689A10
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                     Center clone name: 689_A_10
                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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Research

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                  Lov bp
Lost: gap of 10921 bt
Lost: gap of 10921 bt
Lost: gap of 100 bp
Lost: gap of 100 L
8165 81764: gap of 100 L
85169: ccm-1
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         85269: gap of 100 bp
90445: contig of 5176 bp in length
90545: gap of 100 bp
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3998:
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74167: conf
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40639: gap of 100 by
45518: contig of 4879
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16073: con
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40539: _____
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95008: contig of 4463 bp in length
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23548: contig of 2953
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contig of 3620 k
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37797. .40539
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clone_lib="RPCI-11 Human Male BAC"
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FEATURES
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Clases 1 to 198872)
Cwens,I.S., Gong,Q., Cho,J.W., Huang,T., Potter,C., G
Basu,N.K., Kubota,S., Carvalho,S. and Pennington,M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owens, I.S., Gong, Q., Cho, J.W., Huang, T., Potter, C., Gholami, N., Basu, N.K., Kubota, S., Carvalho, S. and Pennington, M.W. Thirteen UDF glucuronosyltransferase genes encoded at the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rockville Pike, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (10-AUG-2000) Heritable Disorders Branch, NIH-NICHD, 9000
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Homo sapiens UGT1 gene locus, complete sequence.
AF297093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UGT1 locus
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    Conservative
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                                                                                                     'gene-*UGT1A8
                                                                                                                                                              'gene-"UGT1A8"
                                                                                                                                                                                                                             /gene-"UGT1A8"
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                                                                                                                                                                       oin(<34264. .35118,181788. .181919,182603.
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                                                                                                                                                                                                             gene-"UGT1A8"
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codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="UGT1A12p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                ene-"UGT1A12p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="UDP glucuronosyltransferase lAl2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .19887:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 70; 100.0%; Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                         .19978
                                                                                                                                                                                                                                                            .34149
                                                                                                                                                                                                                                                                                                                         .20956
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                 PLDLAVFWYEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKCCA
YGYRKCLGKKGRVKKAHKSKTH"
                                               DQMDNAKRMETKGAGYTLNYLENTSEDLENALKAYINDKSYKENIMRLSSLHKDRPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "gene="UGTIA9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88416. .88427
                                                                                                                                                                                                                                                                                                                                                                                                               'gene="UGTIA9"
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OMDNAKRWETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCOYLFRNALEIASEILOTPVTAYDLYSHTSIWLLRTDFVLDYPKPVHPNMIFIGGIN
CHOGKPLPMEFEAYINASGEHGIVVFSLGSWYSEIPEKKAMAIADALGKIPOTVLWRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene_*ugriA10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEKLILRGHEVVVVMPEVSWOLGKSLNCTVKTYSTSYTLEDLDREFMDFADAOWKAQV
RSLFSLFLSSSNGFFNLFFSHCRSLFNDRKLVEYLKESSFDAVVELDEFDAGGLIVAKY
FSLFSVVFARGIACHYLEEGAQCPAPLSYVPRILLGFSDAMTEKERVRNHIMHLEEHL
FCQYFSKNALEIASEILGTPVTAYDLYSHTSIWLLETDFVLDYPKPVMPNMIFIGGIN
CHOCKPLPMEFEAYINASGEHGIVVFSLGSMVSEIPEKKAMAIADALGKIPQTVLMRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"UDP glucuronosyltransferase 1A10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYRKCLGKKGRVKKAHKSKTH"
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Matches 20
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                             20;
                                                 Similarity
                        Conservative
                                                                                                                               PLFGDQMDNAKRMETKGAGVTLAVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKD
RPVEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITF
                                                                                                                                                                                                     LAKYLSIPAVETLRNIPCDLDEKGTQCPNPSSYIPRLLTTNSDHMTELORVKNMLYPL
ALSYLCHAVSAPYASLASELFQREVSVVDLVSHASVWLFRGDEVMDYPRPIMPNMVFI
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                                                                                                                KCCAYGYRKCLGKKGRVKKAHKSKTH"
                                                                                                                                                                            LWRYTGTRPSNLANNTILYKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              July 129600. .130466,181788. .181919,192603. .182690,
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129525. :12953
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FSLPSVVFARGIFGHYLEEGAQCPAPLSYVPRLLLGFSDAMTEKERVBNHLMHLEEHL
FCPYFFKNVLEIASELLQTPVTAYDLYSHTSIMLLRTDFVLEYPKPVMPNMIFIGGIN
CHQGKPVPMEFEAYINASGEHGIVVFSLGSNVSEIPEKKAMAIADALGKIPQTVLMRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGDOMDNAKRMETKGAGYTLNVLEMTSEDLENALKAVINDKSYKENINRLSSLHKDRP
VEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFKC
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DOMDNAKRÆTKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVE
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VEKLILRGHEYVVVMPEVSWQLGRSLNCTYKTYSTSYTLEDQDREFMYFADARWTAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="UDP glucuronosyltransferase 1A6" protein_id="AAG30420.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene-"UGT1A6"
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104n(98552 ...99406;181788 ...181919,182603 ...182690,
182974 ...183193,187016 ...187313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82974. .183193,187016. .187313)
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/protein_id="AAG30419.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ranslation-"MACLLRSFQRISAGVFFLALWGMVVGDKLLVVPQDGSHWLSMKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roduct="UDP glucuronosyltransferase 1A6" in(109610 .110470,181788 .181919,182603.
                                          100.0%; Score 20; DB 8
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                        ..
                   Mismatches
                                                                DB 89;
                   0
                                                              Length 198872;
              0;
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              Gaps
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AUTHORS
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AF135467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                   Trachypithecus obscurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                      yene, promoter region and partial cds AF135467
                                                                                                                                                                                                                                                         Trachypithecus obscurus UDP-glucuronosyltransferase 1A1 (UGT1A1)
Hall,D., Ybazeta,G., Destro-Bisol,G., Petzl-Erler,M.L. and Di
                           Colobinae; Trachypithecus.
1 (bases 1 to 208)
                                                                                                                                                   dusky leaf monkey
                                                                                                                                                                                                AF135467.1 GI:6456551
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92.0%;

Score 18.4; Pred. No. 5.

DB 89;

Length 200; Indels

0

Gaps

0

0

Mismatches

208 bp

21-NOV-1999

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Db 174939 GTCACGTGACAGAGTCAAAC 174958
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AF135466.1
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-MAR-1999) Human Genetics, E. 57th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variability at the uridine diphosphate glucuronosyltransferase 1A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF135466 200 bp DNA PRI 21-NOV-1999 Promot pygmaeus UDP-glucuronosyltransferase 1A1 (UGT1A1) gene, promoter region and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 200)
Ybazeta,G., Hall,D. and Di Rienzo,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter in human populations and primates Pharmacogenetics (1999) In press
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                                                                                                                                                                                                                                                                                                                                                                                             57th Street, Chicago, IL Location/Qualifiers
          40
/translation="MAVESQGGRPLVLGLLLCVLGPVVSHA"
46 c 62 g 52 t
                                                   /product="UDP-glucuronosyltransferase 1A1"
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/db_xref="GI:6456550"
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/db_xref="taxon:9600"
                                                                                                                                                                                                                                                /product="UDP-glucuronosyltransferase IA1"
                                                                                                                              codon_start=1
                                                                                                                                                        'gene-"UGT1A1"
                                                                                                                                                                                                 'gene-"UGT1A1"
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JOURNAL REFERENCE AUTHORS TITLE

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FEATURES

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234;

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Gaps

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1 gtcacgtgacacagtcaaac 20
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                                                                                                                                                                                                                                       Submitted (18-MAR-1999) Human Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter region and partial AF135462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF135462 234 bp DNA PRI 21-NOV-1999 Pan paniscus UDP-glucuronosyltransferase 1A1 (UGT1A1) gene,
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Wariability at the uridine diphosphate glucuronosyltransferase promoter in human populations and primates

Pharmacogenetics (1999) In press

Chases 1 to 208)

Phazeta,G., Hall,D. and Di Rienzo,A.
                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                           Ybazeta, G., Hall, D. and Di Rienzo, A.
                                                                                                                                                                                                                                                                                           Variability at the uridine diphosphate glucuronosyltransferase 1A1 promoter in human populations and primates Pharmacogenetics (1999) In press 2 (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                                                                Rienzo, A.
                                                                                                                                                                                                                                                                                                                                                                            Hall, D., Ybazeta, G., Destro-Bisol, G., Petzl-Erler, M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan paniscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pygmy chimpanzee.
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                                                                                                                                                                                                                                57th Street, Chicago,
                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 234)
70135104 3501
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                                                                                                                     /gene-"UGTIA1"
                                                                                             /product="UDP-glucuronosyltransferase 1A1" <148: :>234
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                                                                                                                                                           /organism="Pan paniscus"
/db_xref="taxon:9597"
                                                                        gene-"UGTIA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UDP-glucuronosyltransferase 1A1"
<125, .>208
                                              'gene-"UGT1A1"
                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAVESQDRRPLVLGLLLCVLGPVVCHAG"
46 c 60 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="UDP-glucuronosyltransferase
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/db_xref="GI:6456552"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Trachypithecus obscurus"
/db_xref="taxon:54181"
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Pred. No. 5.6;
0; Mismatches
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MUSPC376A MUSPC326A 4201 bp mRNA complete cds.
DEFINITION Nus musculus protein PC376 mRNA complete cds.
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Best Local S
Matches 19
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TITLE
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-MAR-1999) Human Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 234)
Ybazeta,G., Hall,D. and Di Rienzo,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter in human populations and primates Pharmacogenetics (1999) In press
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Mammalia; Eutheria;
1 (bases 1 to 234)
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                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                         /translation="MAVESQGGRPLVLGLLLCVLGPVVSHAGK"
53 c 69 g 62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                           <148. .>234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="UDP-glucuronosyltransferase 1A1"
/protein_id="AAF09173.1"
/protein_id="6456542"
/db_xref="G1:6456542"
/translation="MAYESQGGRPLVLGLLLCVLGPVVSHAGK"
53 c 69 g 62 t
                                                                                                                                                                                                                                                                                                                        /product="UDP-glucuronosyltransferase
/protein_id="AAF09174.1"
/db_xref="GI:6456544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                          /gene="UGT1A1"
148. .>234
                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                            'gene="UGT1A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence and expression of a murine cDNA encoding PC326, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eckhardt, L.A., Laskov, R., Kuehl, W.M., Bergsagel, P.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein PC326.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                        Conservative
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TELEAREVIGAGGGGGISRHYGLEGGEVVEACAVROSMFPYYELEAGEVYEADESSEM
HEETSEDSSEDVEDGESSEN
HEETSEDSSEDVEDIEDSILIDEWIALETSELERFRENDVLGSGGRFVYEAG
GARLFYQRFELEHVFEGHSGCVNTYHFNQHGTLLASGSDDLKVIVWDMLKKSYLNFD
SGHKNNILOAKFLENCNDAILAMCGRDGOVRVAOLSAVAGTHMTKRLVKHGGASHRLG
LEPDSPFRFLITSGEDAVVFNIDLRQAHPASKLLVIKDGAKKVGLTVFVWHDANVYGQFA
VGGDOOFMRIYDORKIDENVNGVLKKFCPHHLLSSDYFAHITSLMYSYDGTELIASY
NDEDIYIFNSSDSDGAQYAKRYKGHRNNSTVKGVYFYGPRSEFVMSGSDCGHIFIWEK
SCOLVQFLEADEGGTINCIDSHPYLPVLASSGLDHEVKNWSPLAEPSKKLAGLKNVI
                                                                                                                                                                /note="putative"
755 c 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"protein pc326"
/protein_id-"AAA39895.1"
/protein_id-"AAA39895.1"
/db_xref-"c120021-
/translation-"MSSHESYTNAAETPENISILSCLGETSGALVDTKTISDIKTMDP
RVSLTPSSDVTGTEDSSVLTPGSTDVNSVDSYGGYEGDDDDEDDKDGDSNLPSL
RVSLTPSSDVTGTEDSSVLTPGSTDVNSVDSYGGYEGDDDDEDDKDGDSNLPSL
                                                                                                                                                                                                                                                                          /gene="protein PC326"
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                                                                                                                                                                                                           'gene-"protein PC326"
                                                                                                                                                                                                                                                     'note-"putative"
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                                                                                                                                                                                                                                                                                                                                                                   rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                              /standard_name="'PC326'"
/note="'20 amino acid repeat'; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INKLKRONFTLRHTSLFNNSMLCFLMSHYTQSÑYGRSWRGIRINAGGGDFSDSSSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="plasma cell"
/tissue_type="plasmacytoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sub_species="domesticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="'member of beta transducin repeat 'mosaic' protein amily'; putative"
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                                                                                                                                                                                                                                                                                                                  te-"putative"
                                                       87.0%;
94.7%;
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AF069716/c
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Cebus apella UDP-glucuronosyltransferase 1A1
promoter region and partial cds.
AF135470
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus. 1 (bases 1 to 207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC F6A4 was sequenced as part of the arabidopsis genome sequencing effort of the Cold Spring Harbor Consortium. For additional information, please see http://www.cshl.org/arabweb. F6A4 overlaps with TIHH towards the centromere. Fingerprint data place F6A4 about 150 kbp to the left of the KNAT3 marker.
Hall, D., Ybazeta, G., Destro-Bisol, G., Petzl-Erler, M.L. and Di
                                                                                                          brown capuchin.
                                                                                                                                                       AF135470.1 GI:6456557
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Genomic Sequence of Arabidopsis Thaliana BAC F6A4, Chromosome IV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF069716 99123 bp DNA PLN 11-JUN-19 Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-JUN-1998) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Parnell,L.D., Huang,E
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Parnell,L.D., Huang,E
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/chromosome="V"
/map="60.5 cM"
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TITLE

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Variability at the uridine diphosphate glucuronosyltransferase 1A1 promoter in human populations and primates

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Best Local Similarity
Matches 18; Conserv
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                                                                  Pharmacogenetics (1999) In press
2 (bases 1 to 207)
Ybazeta,G., Hall,D. and Di Rienzo,A.
Direct Submission
Submitted (18.MAR-1999) Human Genetics, University of Chicago, 924
E. 57th Street, Chicago, IL 60637, USA
Location/Qualifiers
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a
                                                                                                                            Conservative
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90.0%; Pred. No. 52;
tive 0; Mismatches
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                                                                                                                                                       DB 89; Length 207;
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